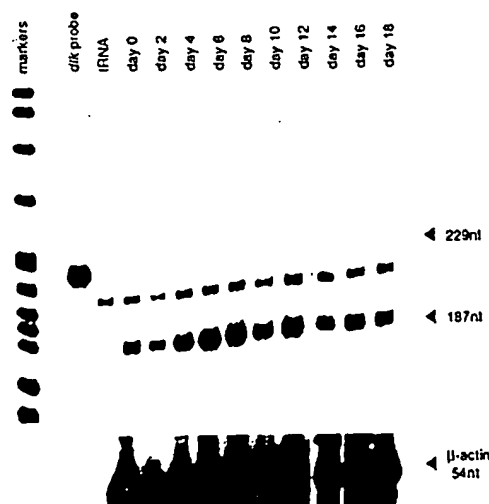




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(54) Title: DEVELOPMENTAL TYROSINE KINASES AND THEIR LIGANDS



(57) Abstract

The invention relates to mammalian receptor tyrosine kinases designated developmental tyrosine kinases (Dtk). Dtk are expressed in multipotential haematopoietic cells, in embryonic stem cells, in brain tissue and in testis, but are not expressed mature lineage-restricted haematopoietic cells. The invention provides full-sequence Dtk as well as extracellular receptor domains of such Dtk. The invention further provides nucleic acid molecules encoding such Dtk, vectors containing DNA encoding such Dtk, ligands which bind to such Dtk, and methods of therapeutic and/or prophylactic treatment employing either the ligands or extracellular receptor domains.

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DEVELOPMENTAL TYROSINE KINASES AND THEIR LIGANDS

FIELD OF THE INVENTION

The present invention generally relates to protein tyrosine kinase receptors widely expressed by early cells of the haematopoietic system, by cells of the neuronal system in brain tissue, and in testis, ligands for such receptors and nucleic acid molecules encoding such receptors.

BACKGROUND OF THE INVENTION

There are several parallels between the development of the haematopoietic and neuronal systems. In particular, the presence of regulatory protein molecules termed growth factors which recognise and bind to specific cell membrane receptors is a common feature of these two systems. It is possible that shared families of receptors exist that are expressed in both early haematopoietic and neuronal stem cells. In turn, there may be a family of proteins which bind these receptors and function as stem cell growth factors.

The current view of vertebrate haematopoietic ontogeny holds that a succession of pluripotential stem cell migrations originate in the yolk sac blood islands, initially invade the hepatic rudiment, and then the spleen and bone marrow. From the bone marrow, a limited number of multipotential stem cells are laid down during embryogenesis that give rise to a much larger population of developmentally restricted progenitor cells, and ultimately produce the mature cells of at least eight cell lineages. The cells of these lineages are classified as red and white blood cells. The white blood cells contain the mature cells of the lymphoid and myeloid systems. Lymphoid cells contain T and B lymphocytes and are derived from pre-T and pre-B cells, respectively. The myeloid system comprises several cell types known as granulocytes, platelets, monocytes, macrophages, and megakaryocytes. The granulocytes are further divided into neutrophils, eosinophils, basophils and mast cells (see review by Metcalf D. The Molecular Control of Blood Cells, Harvard Univ Press, 1988).

5 The haematopoietic system functions by precisely controlling the production of cells in the various lineages. Totipotent haematopoietic stem cells have the ability to both self-renew and differentiate. Stem cells undergo a series of differentiation steps leading to increasingly lineage-restricted progenitor cells. The more mature progenitor cells are restricted to production of only one or two lineages. For some time the colony-forming unit-spleen (CFU-S) assay served to operationally define all stem cells. Recent evidence demonstrates heterogeneity within CFU-S, with only a small fraction of CFU-S capable of contributing to long-term repopulation following ablation of the haematopoietic system by irradiation. It is 10 recognised that stem and progenitor populations are not discrete, but represent a continuum of cells from those of high self-renewal capacity and low probability of differentiation to those cells with low self-renewal probability and high commitment to differentiation. When long-term haematopoiesis is investigated at the clonal level, studies have shown that single stem cell clones are sufficient to 15 maintain haematopoiesis over the lifetime of an animal.

The development of the mammalian embryo is governed by interactions between different embryonic cell populations. This process is manifest at the cellular level in the precise temporal and spatial control of proliferation, differentiation and 20 migration. The coordination of these processes may be achieved in part by the action of a family of regulatory molecules termed growth factors. Growth factors can evoke diverse responses in different cell types and may interact with one another synergistically or antagonistically. Their action is complex and most of our current understanding results from *in vitro* experiments. In most instances, haematopoietic growth factor actions defined *in vitro* have been confirmed *in vivo*. 25 In haematopoiesis, some growth factors are lineage-restricted in their action. These include erythropoietin that acts predominantly on red cell development, and granulocyte colony-stimulating factor that's predominant action is on granulocytes. At the other end of the spectrum is interleukin-3 which can act on several target cells such as granulocyte-macrophage progenitors, eosinophils, megakaryocytes, 30 erythroid cells and mast cells. There are no known growth factors that function exclusively on haematopoietic stem cells.

The ligand for c-kit, termed stem cell factor, kit ligand or mast cell growth factor is the product of the Steel (Sl) locus in mice. The factor acts either alone or synergistically with several known growth factors on primitive stem cells. It is believed that this factor is essential for the development of early haematopoietic stem cells, and cells of the erythroid and mast cell lineages.

The stem cell compartment may be viewed as a finely tuned balance between the action of inhibitors and the stimulatory role of cytokines. As with other stem cell systems, haematopoietic stem cells are distributed in a defined spatial manner within adult bones and not in a random, homogeneous mixture of interacting cell types. A concept that underlies the regulation of haematopoietic stem cell development is that these cells reside within a specialised microenvironment, where the regulatory signals act locally. Stromal cells constitute the bone marrow microenvironment.

Embryonic stem cells are permanent cell lines established directly from the inner cell mass of the preimplantation mouse embryo. They retain the ability to participate in normal embryonic development and, following introduction into the blastocyst, generate chimaeric animals that are mosaic in all tissues. Embryonic stem cells are increasingly being used as cellular vectors for experimentally manipulating the mouse genome.

Doetschman has demonstrated that embryonic stem cells can generate primitive erythroid cells in culture (Doetschman et. al. J. Embryol. Exp. Morphol. 87, 27-45; (1985)). This result was achieved by inducing embryonic stem cells to form cystic embryoid bodies in the presence of preselected batches of human cord serum.

In addition to haematopoietic cell development, it has been noted that neurons also arise in differentiating embryonic stem cells. Haematopoietic differentiation in this system occurred infrequently, slowly and was not synchronized. Recently a modified system enabling the differentiation of embryonic stem cells in methylcellulose into multiple haematopoietic lineages has been described by Wiles

and Keller (Development 111, 259-267, (1991)). Using this approach, macrophages, neutrophils, erythroid cells and mast cells develop in a synchronous manner with high frequency in the absence of human cord serum. The development of haematopoiesis from embryonic stem cells in methylcellulose cultures parallels the onset of haematopoiesis in the developing mouse embryo.

An important objective in the field of developmental biology is the identification of genes, the products of which mediate regulatory signals required during embryogenesis. There is compelling evidence that genes encoding receptor tyrosine kinases (RTKs) are involved in early development in vertebrates. The general family of protein tyrosine kinases can be recognised by the presence of several conserved amino acid regions in the catalytic domain. These conserved regions have been summarised by Hanks et al (Science 241, 42-52, (1988)) and by Wilks et al (Proc. Natl. Acad. Sci. USA 86, 1603-1607, (1989)). The receptor for macrophage colony-stimulating factor *c-fms*, which is important in myeloid cell differentiation and placental development is an RTK. The mouse developmental mutation *W* has been shown to involve an RTK. The *W* locus encodes the c-kit RTK and affects the proliferative and/or migratory properties of primordial germ cells, melanoblasts and haematopoietic stem cells. A recently described RTK termed flk-2, which is related to c-kit, has been isolated using the polymerase chain reaction (PCR) with oligonucleotides to conserved kinase domain motifs. Messenger RNA transcripts for flk-2 are expressed in populations enriched for stem cells and primitive uncommitted progenitor cells, and are absent in mature haematopoietic cells (see Matthews *et al.* Cell 65, 1143-1152, (1991)).

Additional receptor tyrosine kinases expressed on pluripotential haematopoietic stem cells are needed to facilitate the *in vitro* growth of stem cells. The nucleic acid molecules that encode receptor tyrosine kinases expressed by pluripotential stem cells are needed to produce recombinant receptors and ligands.

In vertebrate development, the cells whose descendants give rise to the nervous system are first identified as the neural ectoderm. This forms a tube-like structure beneath the surface of the ectoderm. Following closure of the neural tube some

precursor cells detach from the apical neural tube and form a transient structure called the neural crest. These cells rapidly disperse into the embryo along complex migratory pathways. The proliferating neural crest cells also invade developing tissues such as the skin, gut, and the adrenal gland to form differentiated cell populations within these tissues; eg. melanocytes, enteric neurons and adrenal medullary chromaffin cells.

The diversity of cell types derived from the neural crest poses the problem of how uncommitted embryonic cells acquire particular developmental fates. There are strong parallels between neural crest cell lineage diversification and the process of haematopoiesis. It has been proposed that the earliest neural crest cells should be multipotent and maybe capable of self renewal. Secondly, it should be possible to identify committed progenitors that proliferate symmetrically and are restricted to distinct sublineages and thirdly, there should exist factors which influence the proliferation and/or differentiation of specific types of progenitors (see Anderson Neuron 3, 1-12, (1989)).

Soluble proteins variously termed neurotrophic, growth, and neuronal differentiation factors have been identified that influence the developmental growth, maintenance of function, and plasticity of neuronal populations. These factors have been implicated in the proliferation and differentiation of neurons during embryonic development and in their growth and survival in the adult nervous system. There are a growing number of neurotrophic factors, including nerve growth factor, brain-derived neurotrophic factor, neurotrophin-3 and neurotrophin-4. These molecules constitute a closely related family sharing at least 60% amino acid identity. If the parallel to the haematopoietic system is extended, the range and complexity of cells derived from the neural crest implies that there will be a large number of protein regulators which control this system.

Two different types of receptors have been demonstrated for neurotrophins. One group of these receptors are transmembrane glycoproteins with tyrosine kinase activity encoded by members of the *trk* protooncogene family. It would therefore

be important to isolate additional receptor tyrosine kinases from developing systems such as embryonic stem cells which contain neurons. Ligands for such receptors are required to act inter alia as neurotrophic factors. Nucleic acid molecules encoding the receptors and ligands are needed to produce recombinant
5 receptors and ligands.

It is the object of the present invention to go some way towards fulfilling the above objectives or at least to provide the public with a useful choice.

10 SUMMARY OF THE INVENTION

The present invention has a number of aspects. In a first aspect, the invention provides a mammalian receptor tyrosine kinase which is a developmental tyrosine kinase (Dtk) and which is expressed in multipotential haematopoietic cells, in embryonic stem cells, in brain tissue and in testis, but which is not expressed in
15 mature lineage-restricted haematopoietic cells.

In a further aspect, the invention provides an extracellular receptor domain of a receptor tyrosine kinase as defined above. In preferred embodiments, this extracellular receptor domain can be bound to a support, or can be in a soluble
20 form.

In still a further aspect, the invention provides a nucleic acid molecule encoding a receptor tyrosine kinase or extracellular receptor domain as defined above. This nucleic acid molecule is preferably DNA.
25

In yet a further aspect, the invention provides a vector including a DNA molecule as defined above.

In still a further aspect, the invention provides a method of producing a receptor tyrosine kinase comprising the steps of:
30

- (a) culturing a host cell which has been transformed or transfected with a vector as defined above to express the encoded receptor tyrosine kinase or extracellular receptor domain; and

(b) recovering the expressed receptor tyrosine kinase.

As yet an additional aspect, the invention provides a ligand that binds to a receptor tyrosine kinase as defined above.

5

The ligand can take two forms. In one form, the ligand stimulates the proliferation, differentiation and/or survival of cells which express a receptor tyrosine kinase as defined above (a stimulant ligand).

10

In the second form, the ligand is antagonistic and at least partially blocks or inhibits the function of a receptor tyrosine kinase as defined above through binding to said receptor (an antagonistic ligand).

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In another aspect, the invention provides a method of stimulating the proliferation, differentiation and/or survival of a cell expressing a receptor tyrosine kinase as defined above comprising contacting the cell with a stimulant ligand as defined above.

20

In yet a further aspect, the invention provides a method of inhibiting the function of a receptor tyrosine kinase as defined above comprising contacting the receptor with an antagonistic ligand as defined above.

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In still another aspect, the invention provides a method of treating a disease, syndrome or condition caused or mediated by an excess of a ligand as defined above comprising the step of contacting said excess of said ligand with an effective amount of a receptor tyrosine kinase or an extracellular receptor domain as defined above.

30

In another aspect, the invention provides a method of extracting a ligand from a medium which may contain said ligand comprising the step of contacting said medium with a receptor tyrosine kinase or with an extracellular receptor domain as defined above.

The invention also provides a method of isolating ligand(s) from a medium which may contain said ligand(s), comprising the steps of:

- (a) contacting said medium with an effective amount of a receptor tyrosine kinase or an extracellular domain as defined above;
- (b) detecting which ligand(s) bind; and
- (c) isolating such bound ligand(s).

While the invention broadly consists in the foregoing, it should be appreciated that it also includes the more specific embodiments detailed in the following description:

DESCRIPTION OF THE FIGURES

Figure 1 shows expression of murine Dtk in embryonic stem (ES) cells and embryoid bodies. RNase protection analysis was performed on total RNA (10 μ g) from ESD3 ES cells growing in Leukaemia Inhibitory Factor (LIF) (day 0), or from ES cells maintained in the absence of LIF that were differentiating and developing into cystic embryoid bodies (days 2 to 18). As a control tRNA (10 μ g) was also used. The markers were pBR322 digested with *Msp* I. The size of the free murine Dtk probe was 229 nt. A fully protected fragment representing the presence of murine Dtk transcripts was 187 nt in length. The free β -actin protected fragment is shown in each lane as an RNA loading control.

Figure 2 shows expression of murine Dtk in embryonic mouse tissues. RNase protection analysis was performed on total RNA (10 μ g) isolated from E14.5 embryonic tissues of the C57BL/6J mouse strain. Details of the markers, probes and controls are as described for Figure 1.

Figures 3 and 4 show expression of murine Dtk in adult mouse tissues. RNase protection analysis was performed on total RNA (10 μ g) isolated from the various tissues of adult C57BL/6J mice. Details of the markers, probes and controls are as described for Figure 1.

Figure 5 shows expression of murine Dtk in murine cell lines. The most abundant expression is in the multipotential cell lines FDC-P1 and DA2, and the mast cell line P815. The majority of other cell lines are lineage-committed, mature haematopoietic cell lines, which have very limited murine Dtk expression. The NIH 3T3 cell line is derived from embryonic fibroblasts and C2C12 is a myoblast cell line.

Figure 6 shows the cDNA and amino acid sequence of murine Dtk.

Figure 7 shows the cDNA and amino acid sequence of human Dtk.

DETAILED DESCRIPTION OF THE INVENTION

A. Receptors

In a first aspect, this invention provides a mammalian receptor protein tyrosine kinase (PTK). The mammal in which the PTK exists may be any mammal, such as a mouse, rat, rabbit or human.

Members of the PTK family are recognised by the conserved amino acid regions in the catalytic domains. Examples of PTK consensus sequences have been provided by Hanks *et al.* (Science 241 42-52 (1988), especially Figure 1 starting at page 46) and by Wilks *et al.* (Proc. Natl. Acad. Sci. USA 86, 1603-1607 (1989), especially Figure 2 on page 1605).

Hanks *et al.* identify eleven catalytic subdomains containing PTK consensus residues and sequences. The PTKs of the present invention contain most or all of these consensus residues and sequences.

As indicated above, the PTKs of the invention are receptor PTKs and so are also generally referred to as RTKs. Further, as the applicants believe that the RTKs of the invention are involved in mammalian cell development, they are specifically referred to hereinafter as developmental tyrosine kinases (Dtk).

The Dtk's of the invention are transmembrane receptor tyrosine kinases whose extracellular domains contain two immunoglobulin-like motifs followed by two fibronectin-type III repeats. RTKs of this structure (Axl(Ufo,Ark)) are already known (Janssen *et al.*, Oncogene 6, 2113-2120 (1991); O'Bryan *et al.*, Mol. Cell. Biol 11, 5016-5031 (1991); Rescigno *et al.* Oncogene 6, 1909-1913 (1991); Faust *et al.* Oncogene 7, 1287-1293 (1992)). The Dtk's of the invention are however distinguished from those RTKs having the equivalently structured extracellular domains by their potential function based upon their distribution within the mammalian body.

With regard to this latter feature of the Dtk's of the invention, the applicants have conducted experiments to determine the range of cells in which the developmental tyrosine kinases of the invention are expressed. These experiments were specifically performed in relation to murine Dtk but are believed to be illustrative of the expression of all mammalian Dtk's of the invention.

A.1 Analysis of Murine Dtk expression

The expression of murine Dtk in a range of embryonic and adult mouse tissues was analyzed by ribonuclease protection analysis, using a probe that encompassed sequences encoding the membrane-proximal portion of the extracellular domain of the receptor.

Materials and Methods

1. Embryonic stem cell culture

The ESD3 embryonic cell line (Doetschman *et al.*, J. Embryol. Exp. Morphol. 87 27-45 (1985)) was maintained on gelatin-coated dishes in Dulbecco's-modified Eagle's medium (DMEM) with additives according to established procedures (Hogan *et al.*, Cold Spring Harbour Laboratory, 1-332 (1986)), in the presence of LIF. Cystic embryoid bodies were established following collagenase treatment of the ES cells and subsequent suspension culture in bacteriological-grade petri dishes in DMEM with additives in the absence of LIF (Wiles and Keller, Development 111, 259-265 (1991)).

2. Fetal liver haematopoietic stem cell enrichment

Low density haematopoietic stem cells were isolated from an E14.5 fetal liver cell suspension using equilibrium density centrifugation on a discontinuous metrizamide gradient according to the method of Visser et al., J. Exp. Med., **59**, 1576-1590 (1984). Following this procedure, low density fetal liver cells ($p24 < 1.078 \text{ g/cm}^3$) were incubated for 20 minutes on ice in DMEM medium with $5 \mu\text{g}/10^6$ cells of AA4 monoclonal antibody (rat IgG_{2b}; McKearn et al., Proc. Natl. Acad. Sci. USA, **82**, 7414-7418 (1985)) and washed twice. This antibody has been shown to recognise the most primitive haematopoietic stem cell in fetal liver (Jordan et al., Cell, **61**, 953-963 (1990)). The AA4 labelled cells were then incubated on ice for 20 minutes with magnetic beads conjugated with anti-rat IgG antibody as outlined in the manufacturer's protocol (Advanced Magnetics Corp., Cambridge, MA). Following incubation, AA4⁺ cells were positively-selected on a magnet. Stem cell enrichment was assessed by re-labelling the cells with the AA4 antibody, followed by a second layer antibody staining with goat anti-rat fluorescein isothiocyanate and flow cytometric analysis on a FACS 440 (Becton Dickinson, San Jose, CA).

3. RNA analysis

RNAse protection analysis was performed by hybridization of $10 \mu\text{g}$ of total RNA to RNA probes that encoded sequences of murine Dtk and β -actin, overnight at 52°C . RNAse digestion was performed with RNAse T1 ($1.75 \mu\text{g}/\text{ml}$) and RNAse A ($35 \mu\text{g}/\text{ml}$) at 37°C for one hour. The reaction was stopped with proteinase K ($333 \mu\text{g}/\text{ml}$) and SDS (0.3%). The products were run on a 6% urea/acrylamide gel and the autoradiograph exposed at -70°C . The probe for analysis of Dtk expression was derived from nucleotides 1158 to 1334 of the Dtk sequence, a segment which encodes the membrane-proximal portion of the extracellular domain, and which had been subcloned into pGEM-4Z. In an RNAse protection assay, the free probe yielded a 229 nucleotide (nt) band, and Dtk transcripts protected a fragment of 187 nt. A riboprobe was also constructed from a Sal I-Sma I fragment of human β -actin. The length of the free β -actin probe was 132 nt and β -actin transcripts protected a 54 nt fragment.

Results

1. Embryonic stem cells

Figure 1 demonstrates the expression of Dtk transcripts in both totipotent ES cells growing in LIF (termed day 0), and in differentiating cystic embryoid bodies growing in the absence of LIF for up to 18 days. In this developmental system Dtk is expressed almost uniformly from days 0 to 18, indicated by the presence of a protected 187 nt band for each RNA analyzed. The two bands of approximately 220 nt and 210 nt present in lanes for each RNA sample analyzed are also present in the tRNA lane and are regarded as nonspecific. Of considerable interest with regard to the importance of this receptor in mouse development is the demonstration of Dtk expression in totipotent ES cells. The ES cells from which RNA was extracted for day 0 analysis were selected from cultures, following morphological assessment by phase-contrast microscopy to confirm that they were undifferentiated.

2. Embryonic tissues

Expression of Dtk was detected in total RNA isolated from a wide range of mid-gestational E14.5 embryonic mouse tissues including the brain, eye, thymus, lung, intestine, forelimb, hindlimb and testis (Figure 2). There was limited expression in heart and unfractionated liver.

Figure 2 shows enrichment of Dtk transcripts in E14.5 fetal liver low density AA4⁺ haematopoietic stem cells. Following density-gradient centrifugation and positive selection, the cells used for RNA analysis were greater than 95% AA4⁺, as assessed by flow cytometry (data not shown). Dtk expression was also detected in day 14.5 placenta.

3. Adult tissues

In contrast to the widespread expression of Dtk in embryonic tissues, the pattern of expression in adult tissues becomes restricted (Figures 3 and 4). Dtk transcripts were most abundant in brain, esophagus, bladder, testis, and ovary. In brain, expression of Dtk (relative to β -actin) was more abundant in adult than in embryonic tissue. Adult tissues which contained less abundant, but detectable

transcripts were lung, and regions of the gastrointestinal tract including the stomach and both the small and large intestine. Tissues in which Dtk transcripts were undetectable or expressed at extremely low levels included the salivary gland, thymus, heart, liver, skeletal muscle, kidney, spleen, bone marrow, adrenal gland and uterus.

4. Murine cell lines

The pattern of expression of Dtk in murine cell lines was analyzed in relation to the following: WEHI-3B, 416B, EL4, SO3, SP2/0, P388D₁, P815, FDC-P1, DA2, FDC-P1/IL-2 ras, NIH3T3 and C2C12. The results are shown in Figure 5.

As can be seen from Figure 5, the results are consistent with those above, with the most abundant expression being in the multipotential cell lines FDC-P1 and DA2, and in mast cell line P815. Significant expression is also observed in myoblast cell line C2C12.

In contrast, the remaining cell lines (lineage-restricted mature haematopoietic cell lines) show very limited murine Dtk expression.

From this analysis, the applicants have derived the condition defining the Dtk of the invention - they are expressed in multipotential haematopoietic cells, in totipotent embryonic stem cells, in brain tissue and in testis, but not in mature lineage-restricted haematopoietic cells.

For the purpose of this specification, a multipotential haematopoietic cell is an early haematopoietic cell. Examples of multipotential haematopoietic cells include multipotential factor-dependent cells that have the capacity to proliferate and differentiate into mature haematopoietic cells. In contrast, a mature haematopoietic cell is non self-renewing and has limited ability to give rise to multiple cell lineages. Mature lineage-restricted haematopoietic cells, for the purposes of this specification, are therefore represented by haematopoietic cell lines of the T or B lymphoid lineage or mature myeloid lineages.

The Dtk of the present invention may or may not be expressed in intermediate cells poised between the state of being multipotential and mature.

5 In terms of brain tissue, the Dtk of the invention are primarily expressed in neuronal cells.

In terms of testis, the Dtk are primarily expressed in the Sertoli cells.

10 It will of course be appreciated by those persons skilled in this art that the reference to the Dtk of the invention not being expressed in mature lineage-restricted haematopoietic cells is in a biological context and does not mean that there is absolutely no expression of the Dtk in these cells. As is apparent from Figures 1 to 5, what is meant by the phrase "not expressed in mature-lineage
15 restricted haematopoietic cells" is that there is no significant expression of the Dtk in the cell, i.e. that expression is either undetectable or at an extremely low level.

20 The restricted expression of the Dtk of the invention to cells representative of early multipotential cells, with substantial absence of expression in lineage-restricted cells such as T or B lymphocytes, is consistent with this receptor functioning and transducing signals from the microenvironment to the haematopoietic stem cell compartment. The expression of the Dtk in embryonic stem cells and in some fetal tissues such as brain is also consistent with this receptor and its ligand having a functional role in the specification of cell lineages during embryonic development, including neuronal development. Furthermore,
25 the receptor and its ligand is likely to have a role in the maintenance of function and plasticity in neuronal populations or their derivatives. Finally, the expression of the receptor in adult brain is consistent with the receptor and its ligand having a role in the growth and survival of neurons in the adult nervous system.

30 The embryonic stem cell and haematopoietic multipotential cell line mRNA for Dtk migrates relative to 28S and 18S ribosomal bands on formaldehyde agarose gels at approximately 4.2 Kb. In adult brain tissues, Dtk mRNA migrates at approximately 4.2 Kb.

The Dtk of the invention can usefully be provided in a number of different forms. These include the Dtk itself, the "mature" form of the Dtk, and the extracellular receptor domain of the Dtk.

5 The "mature" form of the Dtk of the invention is the Dtk less its native amino-terminus leader or signal sequence, whereas the extracellular receptor domain is the Dtk lacking the transmembrane region and catalytic domain.

10 The extracellular domain may be identified through commonly recognised criteria of extracellular amino acid sequences. The determination of appropriate criteria is known to those skilled in the art, and has been described, for example by Hopp et al., Proc. Natl. Acad. Sci. USA 78, 3824-3828 (1991); Kyte et al., J. Mol. Biol. 157, 105-132 (1982); Emini, J. Virol 55, 836-839 (1985); Jameson et al. CA BIOS 4, 181-186 (1988); and Karplus et al. Naturwissenschaften 72, 212-213 (1985).

15 Amino acid domains predicted by these criteria to be surface exposed are characteristic of extracellular domains.

20 The Dtk of the invention or their extracellular receptor domains may be prepared by methods known in the art. Such methods include protein synthesis from individual amino acids as described by Stuart and Young in "Solid Phase Peptide Synthesis", Second Edition, Pierce Chemical Company (1984). It is however preferred that the Dtk and/or their extracellular receptor domains be prepared by recombinant methods as will be detailed hereinafter.

25 A.2 Specific Dtk of the Invention

A.2.1 Murine Dtk

30 As is indicated above, a first Dtk of the invention, murine Dtk, has been identified in certain tissues of the mouse. Murine Dtk generally has the nucleic acid and deduced amino acid sequence shown in Figure 6. Figure 6 represents individual amino acid residues as single letters as follows:

	Amino Acid	Three-letter abbreviation	One-letter symbol
5	Alanine	Ala	A
	Arginine	Arg	R
	Asparagine	Asn	N
	Aspartic acid	Asp	D
	Asparagine or aspartic acid	Asx	B
10	Cysteine	Cys	C
	Glutamine	Gln	Q
	Glutamic Acid	Glu	E
	Glutamine or glutamic acid	Glx	Z
	Glycine	Gly	G
15	Histidine	His	H
	Isoleucine	Ile	I
	Leucine	Leu	L
	Lysine	Lys	K
	Methionine	Met	M
20	Phenylalanine	Phe	F
	Proline	Pro	P
	Serine	Ser	S
	Threonine	Thr	T
	Tryptophan	Trp	W
25	Tyrosine	Tyr	Y
	Valine	Val	V

Details of the sequence of murine Dtk are as follows.

30 Sequence Analysis of the Murine Dtk

Figure 6 shows the 3.919 Kb nucleotide and deduced amino acid sequence for murine Dtk from murine neonatal brain. Within the 5' region, a potential site for translation initiation (-GGAGCATGGGG-) is found within a good Kozak consensus sequence. The first methionine initiates an open reading frame of 874
 35 amino acids. Using the method of von Heijne Sequence Analysis in Molecular Biology 113-117, San Diego, Academic Press (1987), the signal cleavage site is predicted to be between alanine 24 and alanine 25, which specifies a 24 amino

acid hydrophobic leader sequence and a mature receptor tyrosine kinase protein of 850 amino acids. Amino acids AGLK to PHSR form a 386 amino acid extracellular domain. A 25 amino acid hydrophobic region from TSWV to LILL is consistent with that of a transmembrane domain (Fasman and Gilbert, Trends Biochem 15, 89-92 (1990)), while the remaining amino acids ending HSSC comprise the cytoplasmic domain.

The extracellular domain of murine Dtk contains eight consensus sites (NxT or S) for N-linked glycosylation, predicting that the mature Dtk protein is glycosylated.

Within the extracellular domain, two repeating protein motifs are identifiable. Using the predictive methods of Williams and Barclay, Ann. Rev. Immunol 6, 381-405 (1988), two C-type immunoglobulin (Ig)-like domains are present from amino acids KLMG to GEET (Ig-like domain I) and FFTV to NIKG (Ig-like domain II). The first Ig domain has a structure similar to a C1 domain, while the second Ig domain is more C2-like. Based on the analysis of Petersen *et al.*, Proc. Natl. Acad. Sci. USA 80, 137-141 (1983), there are two fibronectin type III modules present from amino acids PPAA to PYGD (domain I) and from amino acids PFQT to SHDH (domain II).

Analysis of the 439 amino acid cytoplasmic domain sequence of murine Dtk shows many of the motifs which are highly conserved within the catalytic kinase domain of protein tyrosine kinases (Hanks *et al.*, Science 241, 42-52 (1988)). The motifs GKGEFG and VAVK, which function as the Mg^{2+} -ATP binding site (Ullrich and Schlessinger, Cell 61, 203-212 (1990); Cantley *et al.*, Cell 64, 281-302 (1991)), are observed at the start of the kinase domain. Further towards the carboxy-terminus

of Dtk other conserved kinase motifs are identifiable, including the motif IHRDLAARN, the DFG triplet motif and the motifs KWLALES and DVWAFG. Alignment of the kinase domain of Dtk with other protein tyrosine kinase domains including that of Ufo, suggests there is a kinase insert region specified by the amino acids RIGENPFN. There are 12 tyrosine residues within the cytoplasmic domain of Dtk, including two residues located near the C-terminus that are nested within sequences that exhibit strong homology to Src homology 2 (SH2) domain binding sites (Songyang et al., Cell 72, 767-778 (1993)). One of these sequences, EEVYDLM, is a putative binding site for phosphatidylinositol 3-kinase, but lies within the catalytic domain proper and is unlikely to be autophosphorylated. The sequence DPLYINI fulfills criteria for either a Sem5/Grb2 binding site or a phospholipase C- γ binding site (Songyang *et al.*, (1993)) supra, and its position in the C-terminal tail makes it a good candidate for phosphorylation.

In specific aspects, the invention provides murine Dtk, mature murine Dtk and the extracellular receptor domain of murine Dtk.

Murine Dtk has the amino acid sequence given as SEQ ID NO 1.

Mature murine Dtk has the amino acid sequence given as SEQ ID NO 2.

The extracellular receptor domain of murine Dtk has the amino acid sequence given as SEQ ID NO 5.

The invention also includes functional equivalents of murine Dtk, mature murine Dtk and the extracellular receptor domain of murine Dtk as is described hereinafter.

5 A.2.2 Human Dtk

A second Dtk of the invention has been identified from human tissue. This second receptor is the human homologue of murine Dtk having all of the structural features of murine Dtk.

10 The nucleic acid and deduced amino acid sequence for this receptor tyrosine kinase, hereinafter called "human Dtk", is shown in Figure 7. Sequence details are as follows.

Sequence Analysis of the Human Dtk

15 Figure 7 shows the 4.364 Kb nucleotide and deduced amino acid sequence for the human Dtk from human fetal brain. The structural features of human Dtk closely parallel those described for murine Dtk. The signal peptide encompasses amino acids MGRP to ESAA. The mature protein extends from residues AGLK to HSSC. Within the mature protein the extracellular domain is defined by residues
20 AGLK to PHSR, the transmembrane domain by residues TSWV to LILL, and the cytoplasmic domain from residues RKRR to HSSC.

The extracellular domain contains two repeating protein motifs made up of two immunoglobulin domains (KLMG to GGET and FFTV to NLKG), followed by
25 two fibronectin type III modules (LPAA to PYAD and PFQT to SHDR). The

protein tyrosine kinase domain is encompassed by the amino acids LGKG to RMEL within the cytoplasmic domain. The motifs defined within the murine protein tyrosine kinase domain are also identifiable within the human protein tyrosine kinase domain.

5

Once again, in its specific aspects the invention provides different forms of the Dtk (human Dtk, "mature" human Dtk and the extracellular receptor domain of human Dtk).

10 Human Dtk has the amino acid sequence given as SEQ ID NO 3.

Mature human Dtk has the amino acid sequence given as SEQ ID NO 4.

15 The extracellular receptor domain of human Dtk has the amino acid sequence given as SEQ ID NO 6.

Once again, the invention further includes functional equivalents of human Dtk, mature human Dtk and of the extracellular receptor domain of human DTK.

20 A.2.3 Other Mammalian Dtks

In addition to the murine and human Dtk described above, the invention includes within its scope Dtk of other mammals. Such Dtk are the homologues of both murine and human Dtk and can be readily identified by those persons skilled in the art with reference to the characterising data given above for murine Dtk and

25 human Dtk.

By way of example, one method for identifying other Dtk of the invention involves the formation of a DNA library from a suitable tissue source (such as brain) obtained from the mammal. This library can then be screened to identify DNA coding for homologues to murine Dtk and human Dtk as will be described in more detail below.

B. Nucleic Acid Molecules Encoding the Dtk of the Invention

In another aspect of this invention, the applicants provide nucleic acid molecules encoding the Dtk. These nucleic acid molecules may be DNA (isolated from nature, synthesised or cDNA) or RNA. Most often, the nucleic acid molecules will be DNA.

B.1 Nucleic Acid Molecules Encoding Murine Dtk and Human Dtk

As indicated above, the nucleic acid sequences for murine Dtk and human Dtk have been determined. In specific aspects, the invention therefore provides nucleic acid molecules (in the form of DNA) as follows:

1. A DNA molecule encoding murine Dtk having the nucleotide sequence given as SEQ ID NO 7.
2. A DNA molecule encoding mature murine Dtk having the nucleotide sequence given as SEQ ID NO 8.
3. A DNA molecule encoding the extracellular receptor domain of murine Dtk having the nucleotide sequence given as SEQ ID NO 11.

4. A DNA molecule encoding human Dtk having the nucleotide sequence given as SEQ ID NO 9.
5. A DNA molecule encoding mature human Dtk having the nucleotide sequence given as SEQ ID NO 10.
6. A DNA molecule encoding the extracellular receptor domain of human Dtk having the nucleotide sequence given as SEQ ID NO 12.

The invention also includes within its scope functional equivalents of these DNA molecules.

B.2 Nucleic Acid Molecules Encoding Dtk of other Mammals

It will be appreciated that DNA molecules encoding the functional equivalent homologues of murine Dtk and human Dtk from other mammals are also within the scope of the invention. Such DNA molecules can be readily identified using conventional techniques and with reference to the information contained herein characterising murine Dtk and human Dtk.

By way of generic illustration, DNA molecules encoding homologues of murine Dtk and human Dtk in other mammals can be identified by employing the following general steps:

(a) Formation of a cDNA library:

Total mRNA from a suitable tissue source (such as brain) of the mammal is prepared by standard procedures (Ausubel et al, (Eds),

"Current Protocols in Molecular Biology" Greene Associates/Wiley Interscience, New York (1990)), and cDNA synthesised. A cDNA library is formed (for example in λ ZAP II).

5 (b) Library Screening:

The cDNA library formed as above is screened for the presence of cDNA encoding homologues to murine Dtk and human Dtk.

10 Screening will generally employ a DNA hybridisation or amplification step with the probes or primers being selected based upon the already determined sequences of murine and human Dtk.

15 Most conveniently, the screening procedure will involve DNA amplification using the polymerase chain reaction (PCR) (Saiki et al Science 239, 487 (1988)) with the PCR primers being selected such that highly conserved regions from within the DNA sequence of murine and human Dtk will be within the amplified PCR product.

(c) DNA Isolation and Sequencing:

20 Clones from the cDNA library which are identified by screening step (b) as containing cDNA encoding homologues to murine and human Dtk are selected, and the size of the cDNA insert sourced from the brain determined. Such clone(s) including a cDNA insert of the appropriate size to code for the full-length Dtk are selected and the cDNA insert isolated. Each isolated cDNA insert is then sequenced
25 using known procedures (for example, using the standard

dideoxy chain-termination method of Sanger et al., Proc. Natl. Acad. Sci. USA 74, 5463-5467 (1977)).

B.3 Genetic Mapping of Murine Dtk and Human Dtk

By way of further characterisation of both murine Dtk and human Dtk, the applicants have performed experiments to establish the chromosomes on which the genes coding for these Dtk are located. Details of these experiments are given below.

Materials and Methods

B.3.1 Fluorescent In Situ Hybridization (FISH)

A partial Sau3A genomic DNA library in λ 2001, prepared from mouse ES cells (Boehm et al., Proc. Natl. Acad. Sci. USA 88, 3927-3931 (1991)), was screened with the 3.525 kb cDNA insert purified from pMo23A using methods previously described (Morris, et al., Blood 76, 1812-1818 (1991)). Of 34 positive clones, two of the most intensely hybridizing, λ Mo23A-7.1 and λ Mo23A-8.1, were selected for FISH studies. The pMo23A plasmid, and DNA isolated from bacteriophage clones λ Mo23A-7.1 and λ Mo23A-8.1, were biotinylated by nick-translation using biotin-14-dATP (Bethesda Research Laboratories, Gaithersburg, MD).

Karyotypically normal, 40,XY, mouse metaphase cells were prepared from ES cells in culture using standard procedures. Fluorescent in situ hybridization and detection procedures were essentially as described (Morris et al., Human Genetics 91, 31-36 (1993)), except that mouse Cot 1 DNA (BRL, final concentration 250ng/ μ l) was used to suppress repetitive sequences in the two phage DNA probes. Chromosomes were G-banded using DAPI (4',6-diamidino-2-

phenylindole dihydrochloride, Sigma, St Louis, MO) as a counterstain for fluorescence analysis.

B.3.2 Single-strand conformation polymorphism (SSCP)

5 Primer sequences from the 3' untranslated region of the Dtk cDNA used for genetic mapping were as follows:

DtkMap1 5' TGGATGGCAGTAAGGGAGG 3'

5' CTTAAGAGGGGGCAAACCTGG 3'

10 DtkMap2 5' GCTTAGAGGAGGTGAGCCAGA 3'

5' TGGGCAGTGCTGAGTTCC 3'

PCR was performed using standard conditions with the addition of ^{32}P -labelled dCTP. Specifically, 25 μl reactions were performed in 10 mM-Tris-HCl, 50 mM KCl using 250 ng of genomic DNA, 1 μM of each primer, and 1.4 mM MgCl_2 . This was overlaid with oil, denatured at 94°C for 5 minutes, and transferred to an 80°C heating block. dNTPs were added to a final concentration of 0.2 mM, including 1.25 μCi of [α - ^{32}P]dCTP (1 μl of a 3000 Ci/mmol stock to 8 reactions). 1.25 units of AmpliTaq DNA polymerase (Perkin-Elmer Cetus) was added and cycling conditions were as follows: 58°C annealing reaction for 1 minute, 72°C extension reaction for 2 minutes, and 91°C denaturation for 1 minute. The cycle was repeated 30 times with a final 72°C extension reaction for 5 minutes. SSCP analysis was performed by electrophoresing the single-stranded PCR products on a non-denaturing gel as follows: 2 μl of the PCR reaction was added to 8 μl of USB stop solution (100% formamide containing xylene cyanol and bromophenol blue).

This was denatured for 5 minutes at 94°C and transferred to an ice bucket. 3 μ l was loaded on a 5% non-denaturing acrylamide gel containing 0.5X TBE and no glycerol. This was run in a 4°C cold room in 0.5X TBE at 40 watts constant power for 2-3 hours. The gel was transferred to filter paper, dried, and
5 autoradiographed overnight with an intensifying screen.

Results

The chromosomal localisation of the gene encoding murine Dtk has been established on chromosome 2 band F using fluorescent in situ hybridisation. This
10 result has been confirmed using single strand conformation polymorphism analysis in the BXD recombinant inbred series.

The gene encoding human Dtk has been mapped using fluorescent in situ hybridisation to chromosome 15q15.

C. Recombinant Expression of Dtk of the Invention

In yet another aspect, the present invention relates to the recombinant expression of the Dtk or of their extracellular receptor domains.

20 As will be exemplified below, the nucleic acid molecules that encode the receptors or the extracellular receptor domains of the invention may be inserted into known vectors for use in standard recombinant DNA techniques. Standard recombinant DNA techniques are those such as are described in Sambrook et al.; "Molecular Cloning" 2nd Edition Cold Spring Harbour Laboratory Press (1987) and by

Ausubel et al., Eds, "Current Protocols in Molecular Biology" Greene Publishing Associates and Wiley-Interscience, New York (1987).

Vectors for expressing proteins in bacteria, especially E. coli, are known. Such
5 vectors include the PATH vectors described by Dieckmann and Tzagoloff in J. Biol. Chem. 260, 1513-1520 (1985). These vectors contain DNA sequences that encode anthranilate synthetase (TrpE) followed by a polylinker at the carboxy terminus. Other expression vector systems are based on beta-galactosidase (pGEX); lambda P maltose binding protein (pMAL); and glutathione S-
10 transferase (pGST) - see Gene 67, 31 (1988) and Peptide Research 3, 167 (1990).

Vectors useful in yeast are available and well known. A suitable example is the 2 μ plasmid.

15 Suitable vectors for use in mammalian cells are also known. Such vectors include well-known derivatives of SV-40, adenovirus, retrovirus-derived DNA sequences and vectors derived from combination of plasmids and phage DNA.

Further eucaryotic expression vectors are known in the art (e.g. P.J. Southern and
20 P. Berg, J. Mol. Appl. Genet. 1, 327-341 (1982); S. Subramani et al, Mol. Cell. Biol. 1, 854-864 (1981); R.J. Kaufmann and P.A. Sharp, "Amplification And Expression of Sequences Cotransfected with a Modular Dihydrofolate Reductase Complementary DNA Gene," J. Mol. Biol. 159, 601-621 (1982); R.J. Kaufmann and P.A. Sharp, Mol. Cell. Biol. 159, 601-664 (1982); S.I. Scahill et al, "Expression
25 And Characterization Of The Product Of A Human Immune Interferon DNA

Gene In Chinese Hamster Ovary Cells," Proc. Natl. Acad. Sci. USA 80, 4654-4659 (1983); G. Urlaub and L.A. Chasin, Proc. Natl. Acad. Sci. USA 77, 4216-4220, (1980).

5 The expression vectors useful in the present invention contain at least one expression control sequence that is operatively linked to the DNA sequence or fragment to be expressed. The control sequence is inserted in the vector in order to control and to regulate the expression of the cloned DNA sequence. Examples of useful expression control sequences are the lac system, the trp system, the tac system, the trc system, major operator and promoter regions of phage lambda, the control region of fd coat protein, the glycolytic promoters of yeast, e.g. the promoter for 3-phosphoglycerate kinase, the promoters of yeast acid phosphatase, e.g. Pho5, the promoters of the yeast alpha-mating factors, and promoters derived from polyoma, adenovirus, retrovirus, and simian virus, e.g. the early and late promoters or SV40, and other sequences known to control the expression of genes of prokaryotic and eucaryotic cells and their viruses or combinations thereof.

Vectors containing the receptor-encoding DNA and control signals are inserted into a host cell for expression of the receptor. Some useful expression host cells include well-known prokaryotic and eucaryotic cells. Some suitable prokaryotic hosts include, for example, E. coli, such as E. coli SG-936, E. coli HB 101, E. coli W3110, E. coli X1776, E. coli X2282, E. coli DHT, and E. coli MR01, Pseudomonas, Bacillus, such as Bacillus subtilis, and Streptomyces. Suitable eucaryotic cells include yeast and other fungi, insect, animal cells, such as COS cells and CHO cells, human cells and plant cells in tissue culture.

A specific although non-limiting example of this aspect of the invention is set out below. It will be appreciated that while the expression of murine Dtk is exemplified, the procedures disclosed are equally applicable to the expression of other Dtk's, or to the expression of extracellular receptor domains of such Dtk's.

5

C.1 Expression of cloned murine Dtk in heterologous cell lines

The coding region of murine Dtk was ligated in-frame into the commercially available expression vector pcDNA3 (InVitrogen) using standard molecular biology techniques. The pcDNA3-Dtk construct was electroporated into several heterologous cell lines to demonstrate expression of Dtk. Electroporation, drug selection and isolation of Dtk-expressing clones for each cell line followed standard techniques (in M. Kriegler, "Gene Transfer and Expression - A Laboratory Manual", Stockton Press, New York 1990).

The Dtk construct was expressed in the factor-dependent cell lines FDC-P1, BAF/3 and 32D, and in the NIH 3T3 cell line (all commercially available). The expression of Dtk in these cell lines has been ascertained at the level of RNA using standard techniques for the isolation of RNA and its detection using radiolabelled Dtk probes which are familiar to those experienced in the field (see Sambrook et al., "Molecular Cloning," Second Edition, supra vide).

20

D. Ligands

The invention also includes ligands that bind to the Dtk's of the invention.

The ligand may be a protein such as a growth factor that occurs naturally in a mammal, preferably the same mammal that produces the corresponding Dtk. The growth factor may be isolated and purified, or be present on the surface of an isolated population of cells, such as stromal cells.

5

The ligand may also be a molecule that does not occur naturally in a mammal. For example, antibodies raised against the receptors of the invention or against anti-ligand antibodies mimic the shape of, and act as, ligands if they constitute the negative image of the receptor or anti-ligand antibody binding site.

10

Such antibodies may be polyclonal but are preferably monoclonal. Monoclonal antibodies may be produced by methods known in the art. These methods include the immunological method described by Kohler and Milstein in Nature 256, 495-497 (1975) and Campbell in "Monoclonal Antibody Technology, the Production and Characterization of Rodent and Human Hybridomas" in Burdon et al. Eds, Laboratory Techniques in Biochemistry and Molecular Biology, Volume 13, Elsevier Science Publishers, Amsterdam (1985); as well as by the recombinant DNA method described by Huse et al. in Science 246, 1275-1281 (1989).

15

20 In yet another form, the ligand may also be a non-protein molecule that acts as a ligand when it binds to, or otherwise comes into contact with, the receptor.

25 In addition, ligands may be of two functional types. The first functional type of ligand is a molecule which binds to the receptor and stimulates it in performing its normal function (a "stimulant ligand"). The second functional type of ligand is a

molecule which binds to the receptor and inhibits or prevents it performing its normal function (an "antagonistic ligand").

Both types of ligand will find application in either therapeutic or prophylactic treatments as described below.

D.1 Sources of Ligands

The strategy for isolating a ligand for the Dtk of the invention is based on the assumption that the ligand will either be a soluble, secreted protein or alternatively it will be membrane-bound or associated.

To screen for soluble ligands, conditioned media from a range of tumor cell lines and tissues can be used. Such cell lines are readily available from the American Type Culture Collection (ATCC) Rockville, Maryland, USA. Conditioned media is generated from these cell lines using a variety of culture and induction protocols. The cell lines are grown using standard tissue culture techniques which are detailed by ATCC for each cell line. Conditioned medium from tissues is generated by growing minced tissue fragments in culture medium for a defined time period.

To screen for membrane-associated ligands a different approach is taken. Cell lines in which from tissues which are in close proximity to those cells or tissues which have been shown to express the Dtk receptor are used. This approach is based on the likelihood of close cell-to-cell contact between receptor-expressing cells and ligand-expressing cells. An example of this is in the testis where Sertoli

cells express the receptor, while germ cells are considered a likely source of membrane-bound ligand. A further example in the brain would be where one type of neuron expresses the receptor, while microglial cells or another non-neuronal brain cell are considered likely to express the ligand.

5

D.2 Ligand Screening Procedures

In illustrating the screening procedures, reference will be made to murine Dtk as representative of the Dtk of the invention. Equivalent procedures can of course be employed in screening protocols using other mammalian Dtk such as human Dtk or the extracellular receptor domains of such Dtk.

10

Two approaches are followed to screen for the ligand for murine Dtk. If the ligand is soluble, assays which utilise either growth responses or changes in tyrosine phosphorylation will be used. Alternatively, if the ligand is membrane-bound, ligand-expressing cells will be detected using a Dtk-tag protein system whereby the extracellular domain of Dtk is fused with sequence encoding part of the human immunoglobulin molecule, such as the Fc region or the μ chain. The tag can then be detected using reagents which bind to the tag, such as Protein A-alkaline phosphatase or Protein A-radioiodine¹²⁵.

15

20

D.3 Soluble ligand

To detect soluble ligand in the media conditioned by tumor cell lines or tissues, a range of concentrations of this media are added to one of the factor-dependent cell lines described above, that have been transfected with, and express the Dtk receptor. These cell lines are routinely maintained in interleukin-3 containing

25

tissue culture medium. By withdrawing this medium and adding sources of potential ligand for Dtk, a growth response will be sought that is mediated via the introduced Dtk receptor. This response can be detected using the uptake of radiolabelled thymidine and counting this uptake by liquid scintillation spectroscopy. These techniques are standard for those familiar in the art (see Kriegler (supra); and Crosier et al., Proc. Natl. Acad. Sci. USA 88: 7744-8 (1991)).

An alternative detection system for ligands contained in tumor cell line conditioned medium uses the Dtk-expressing NIH 3T3 cell line as an indicator system, in conjunction with monitoring alterations in tyrosine phosphorylation of the Dtk receptor. Conditioned medium that contains the ligand for Dtk will trigger activation of the receptor which in turn is reflected in the phosphorylation status of the receptor. The system uses standard techniques whereby the NIH 3T3 cells are incubated with conditioned medium, cell lysates produced which in turn are immunoprecipitated with an anti-murine Dtk polyclonal antibody, proteins are resolved on SDS-PAGE gels, followed by transfer to nitrocellulose filters and subsequent Western blotting with an anti-phosphotyrosine antibody and detection using enhanced chemiluminescence techniques. These techniques are standard protein biochemistry methods (see B. Sefton and T. Hunter (eds), "Methods in Enzymology," vol 200 and 201, 1990; and Amersham, Manufacturer's protocols for ECL techniques). The expected result with this technique would be that potential ligand-containing media would stimulate increased tyrosine phosphorylation, compared with background levels detected in these cells.

D.4 Membrane-bound ligand

Screening for membrane-bound or associated ligands for the Dtk receptor relies on the use of a Dtk-tag fusion protein detection system. The extracellular domain of the Dtk receptor is fused in-frame to the Fc region of human immunoglobulin (IgG) or to part of the human μ chain of IgM. This procedure follows that described by Goodwin et al., Cell 73: 447-456 (1993). The fusion protein is produced by transfecting the fused genes contained within the expression pED δ c vector into COS cells. The fusion protein is purified on Protein A-Sepharose columns (Pharmacia). The Dtk-tag fusion proteins are biotinylated using sulfosuccinimidyl-6-biotinamido)-hexanoate (Pierce Chemicals) according to the manufacturer's procedures. Alternatively, FITC-conjugated Dtk-tag fusion protein is generated by conjugating the fusion protein to FITC using standard techniques (see Suda et al., Cell 75: 169-1178, 1993).

The Dtk-tag fusion protein is used to screen for the expression of bound Dtk protein on tumor cell lines using flow cytometric techniques. The techniques used for the labelling of cells and flow cytometric analysis follow those described by Mosley et al., Cell 59: 335-348 (1989). Tumor cells are labelled on ice with the biotinylated Dtk-fusion protein using avidin-FITC, or the FITC-labelled protein is used directly in FACS analysis. The screening procedure is aimed at detecting a cell line that produces a signal above background with the Dtk-tag fusion protein, compared with an unrelated receptor-tag fusion protein. Sequential FACS sorting of Dtk ligand-expressing cells is undertaken to generate a high Dtk ligand-expressing tumor cell subline which can be used for the generation of a cDNA

expression library (for an overview of this strategy see Wong in Genetic Engineering Vol. 12, ed by J K Setlow, 1990).

E Expression Cloning of the Dtk Ligand

5 E.1 Construction of an expression library

A random-primed expression library is constructed from poly(A)⁺ mRNA isolated from the cell line or tissue demonstrated to give a positive signal in either the growth assay, phosphorylation assay or Dtk-tag fusion protein assay outlined above. The techniques used for construction of the expression library are standard
10 procedures for those experienced in the field (see McMahon et al., EMBO J. 10, 2821-2832, 1991; and Kriegler (supra)).

E.2 Cloning of the murine or human Dtk ligand

The expression library constructed from the cell line or tissue is screened by
15 transfecting pools of cDNAs into COS cells using standard techniques (see Sambrook et al., supra). Two approaches are used to detect positive pools, depending on whether there has been evidence for either a soluble form of ligand or a membrane-bound form of ligand.

20 *Soluble forms:* COS supernatants are screened in the detection systems outlined above for soluble ligand forms. COS cells are grown in 10 cm plates using standard tissue culture techniques.

Membrane-bound forms: COS cells are grown in LabTech (Nunc) chambers and
25 positive pools are detected by using the binding of Dtk-tag fusion protein to the

COS cells, followed by detection with either a Protein A-horseradish peroxidase enzymatic reaction or Protein A-¹²⁵I binding and subsequent autoradiography.

Procedures for the breaking down of cDNA pools, subsequent sib selection and the isolation of single cDNA clones are outlined in Sambrook et al., (supra) and Wong (supra). Sequence analysis of single cDNAs follows standard techniques. Once a single cDNA clone is isolated this is transfected into COS cells or into CHO cells for large scale production of protein using standard procedures.

F Application of Ligands for the Dtk of the Invention

The types of ligand discussed above can be employed in two distinctive methods in accordance with this invention.

The first such method is a method of stimulating the proliferation, differentiation and/or survival of a cell expressing a Dtk of the invention. This stimulation, which can occur *in vivo* or *ex vivo*, involves contacting the cell with an effective amount of the ligand.

The ability of a ligand according to the invention to stimulate cells such as stem cells which express the Dtk of the invention has important therapeutic applications. Such applications include medically treating mammals, including humans, whose stem cells do not sufficiently undergo self-renewal. Examples of such medical problems which can be treated in this way include those that occur when defects in haematopoietic stem cells or their related growth factors depress the number of blood cells, leading to disorders such as aplastic anaemia. The

treatment of bone marrow damage resulting from cancer chemotherapy and radiation is another example of a medical problem that could be treated in this way.

5 The method can also be applied in stimulating the proliferation, differentiation and/or survival of mammalian fetal or adult neuronal cells or cells that form part of the central nervous system. Again, this has important therapeutic applications. Such applications include treating mammals, including humans, for inherited or degenerative disorders of the central nervous system. An additional application is
10 the treatment of individuals with central nervous system trauma, for example, spinal cord trauma resulting from either crushing or asphyxia.

Yet a further therapeutic application for the ligands of the invention is in sports medicine, particularly in the treatment of muscle injuries. The Dtk of the
15 invention is abundantly expressed on myoblast cells but not on mature muscle cells. Application of the ligand will stimulate myoblast cell proliferation and differentiation, leading to muscle repair.

In terms of *ex vivo* applications, the method has implications for gene therapy. In
20 gene therapy genes are inserted into host cells (such as haematopoietic stem cells and myoblasts) and the expression of the gene regulated by either an endogenous or an exogenous promoter. However, it is often difficult to maintain growth and survival of these cells *ex vivo* while they are being manipulated for the insertion of foreign genes. Therefore, as the Dtk of the invention is expressed on
25 haematopoietic stem cells and myoblasts, the ligand has a direct application in

stimulating the growth, proliferation or simple survival of their cells during the manipulative process.

5 The second distinct method of the invention is a method of inhibiting the function of the Dtk of the invention. This method, which would normally be applied *in vivo* for both prophylactic and therapeutic applications, involves contacting the receptor with a ligand which blocks or prevents stimulation of the receptor (an antagonist ligand).

10 In terms of prophylaxis, such a method has specific application to the Sertoli cells of the testis, which abundantly express the receptor. Due to the involvement of these Sertoli cells in male fertility, contacting the receptors with an antagonistic ligand has a potential application in the control of male fertility including in male contraception.

15 A potential therapeutic application of contacting cells expressing the Dtk of the invention with an antagonistic ligand is in anti-tumour therapy. This potential application arises from the growing understanding of the role sometimes played by RTKs in tumour formation.

20 G Therapeutic Applications of Soluble Receptors

The extracellular receptor domain of the invention as described above also have potential therapeutic applications. Such applications are in a method of treating a disease, syndrome or condition caused or mediated by an excess of a ligand of the invention (whether stimulant or antagonistic).

25

In this method, the extracellular receptor domain of the Dtk in a soluble form can be used as a molecular "sponge" or "sink" to remove the excess of the ligand or at least to block its activity.

5 H Functional Equivalents

The invention includes functional equivalents of the Dtk, receptor domains, nucleic acid molecules and ligands described above.

10 The Dtk, extracellular receptor domains and ligands are or include proteins. A protein is considered a functional equivalent of another protein for a specific function if the equivalent protein is immunologically cross-reactive with, and has the same function as, the original protein. The equivalent may, for example, be a fragment of the protein, or a substitution, addition or deletion mutant of the protein.

15

For example, it is possible to substitute amino acids in a sequence with equivalent amino acids using conventional techniques. Groups of amino acids known normally to be equivalent are:

- 20 (a) Ala(A) Ser(S) Thr(T) Pro(P) Gly(G);
 (b) Asn(N) Asp(D) Glu(E) Gln(Q);
 (c) His(H) Arg(R) Lys(K);
 (d) Met(M) Leu(L) Ile(I) Val(V); and
 (e) Phe(F) Tyr(Y) Trp(W).

Substitutions, additions and/or deletions in the receptors and ligands may be made as long as the resulting equivalent receptors and ligands are immunologically cross-reactive with, and have the same function as, the native receptors and ligands.

5

10

The equivalent receptors and ligands will normally have substantially the same amino acid sequence as the native receptors and ligands. An amino acid sequence that is substantially the same as another sequence, but that differs from the other sequence by means of one or more substitutions, additions and/or deletions is considered to be an equivalent sequence. Preferably, less than 25%, more preferably less than 10%, and most preferably less than 5% of the number of amino acid residues in the amino acid sequence of the native receptors and ligands are substituted for, added to, or deleted from.

15

Equivalent nucleic acid molecules include nucleic acid sequences that encode equivalent receptors and ligands as defined above. Equivalent nucleic acid molecules also include nucleic acid sequences that, due to the degeneracy of the nucleic acid code, differ from native nucleic acid sequences in ways that do not affect the corresponding amino acid sequences.

20

Those persons skilled in the art will of course appreciate that the above description is provided by way of example only and that the invention is limited only by the lawful scope of the appended claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(2) TITLE OF INVENTION: Developmental Tyrosine Kinases and their Ligands.

(3) NUMBER OF SEQUENCES: 12

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(B) COMPUTER: IBM PC COMPATIBLE

(C) OPERATION SYSTEM: MS-DOS

(D) SOFTWARE: WORD PERFECT 5.1 FOR DOS

(6) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE: 16-FEBRUARY 1994

(C) CLASSIFICATION

(7) ATTORNEY/AGENT INFORMATION:

(A) NAME: BENNETT, MICHAEL R.

(8) TELECOMMUNICATION INFORMATION

(A) TELEPHONE: (64 4) 473 8278

(B) TELEFAX: (64 4) 472 3358

(2) INFORMATION FOR SEQUENCE ID NO. 1:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 874 AMINO ACIDS

(B) TYPE: AMINO ACID

(C) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: PROTEIN

(3) SEQUENCE DESCRIPTION: SEQ ID NO. 1:

Met	Gly	Trp	Pro	Gly	Leu	Arg	Pro	Leu	Leu	Leu	Ala	Gly	13
Leu	Ala	Ser	Leu	Leu	Leu	Pro	Gly	Ser	Ala	Ala	Ala	Gly	26
Leu	Lys	Leu	Met	Gly	Ala	Pro	Val	Lys	Met	Thr	Val	Ser	39
Gln	Gly	Gln	Pro	Val	Lys	Leu	Asn	Cys	Ser	Val	Glu	Gly	52
Met	Glu	Asp	Pro	Asp	Ile	His	Trp	Met	Lys	Asp	Gly	Thr	65
Val	Val	Gln	Asn	Ala	Ser	Gln	Val	Ser	Ile	Ser	Ile	Ser	78

Glu	His	Ser	Trp	Ile	Gly	Leu	Leu	Ser	Leu	Lys	Ser	Val	91
Glu	Arg	Ser	Asp	Ala	Gly	Leu	Tyr	Trp	Cys	Gln	Val	Lys	104
Asp	Gly	Glu	Glu	Thr	Lys	Ile	Ser	Gln	Ser	Val	Trp	Leu	117
Thr	Val	Glu	Gly	Val	Pro	Phe	Phe	Thr	Val	Glu	Pro	Lys	130
Asp	Leu	Ala	Val	Pro	Pro	Asn	Ala	Pro	Phe	Gln	Leu	Ser	143
Cys	Glu	Ala	Val	Gly	Pro	Pro	Glu	Pro	Val	Thr	Ile	Tyr	156
Trp	Trp	Arg	Gly	Leu	Thr	Lys	Val	Gly	Gly	Pro	Ala	Pro	169
Ser	Pro	Ser	Val	Leu	Asn	Val	Thr	Gly	Val	Thr	Gln	Arg	182
Thr	Glu	Phe	Ser	Cys	Glu	Ala	Arg	Asn	Ile	Lys	Gly	Leu	195
Ala	Thr	Ser	Arg	Pro	Ala	Ile	Val	Arg	Leu	Gln	Ala	Pro	208
Pro	Ala	Ala	Pro	Phe	Asn	Thr	Thr	Val	Thr	Thr	Ile	Ser	221
Ser	Tyr	Asn	Ala	Ser	Val	Ala	Trp	Val	Pro	Gly	Ala	Asp	234
Gly	Leu	Ala	Leu	Leu	His	Ser	Cys	Thr	Val	Gln	Val	Ala	247
His	Ala	Pro	Gly	Glu	Trp	Glu	Ala	Leu	Ala	Val	Val	Val	260
Pro	Val	Pro	Pro	Phe	Thr	Cys	Leu	Leu	Arg	Asn	Leu	Ala	273
Pro	Ala	Thr	Asn	Tyr	Ser	Leu	Arg	Val	Arg	Cys	Ala	Asn	286
Ala	Leu	Gly	Pro	Ser	Pro	Tyr	Gly	Asp	Trp	Val	Pro	Phe	299
Gln	Thr	Lys	Gly	Leu	Ala	Pro	Ala	Arg	Ala	Pro	Gln	Asn	312
Phe	His	Ala	Ile	Arg	Thr	Asp	Ser	Gly	Leu	Ile	Leu	Glu	325
Trp	Glu	Glu	Val	Ile	Pro	Glu	Asp	Pro	Gly	Glu	Gly	Pro	338
Leu	Gly	Pro	Tyr	Lys	Leu	Ser	Trp	Val	Gln	Glu	Asn	Gly	351
Thr	Gln	Asp	Glu	Leu	Met	Val	Glu	Gly	Thr	Arg	Ala	Asn	364
Leu	Thr	Asp	Trp	Asp	Pro	Gln	Lys	Asp	Leu	Ile	Leu	Arg	377
Val	Cys	Ala	Ser	Asn	Ala	Ile	Gly	Asp	Gly	Pro	Trp	Ser	390
Gln	Pro	Leu	Val	Val	Ser	Ser	His	Asp	His	Ala	Gly	Arg	403
Gln	Gly	Pro	Pro	His	Ser	Arg	Thr	Ser	Trp	Val	Pro	Val	416
Val	Leu	Gly	Val	Leu	Thr	Ala	Leu	Ile	Thr	Ala	Ala	Ala	429
Leu	Ala	Leu	Ile	Leu	Leu	Arg	Lys	Arg	Arg	Lys	Glu	Thr	442
Arg	Phe	Gly	Gln	Ala	Phe	Asp	Ser	Val	Met	Ala	Arg	Gly	455
Glu	Pro	Ala	Val	His	Phe	Arg	Ala	Ala	Arg	Ser	Phe	Asn	468
Arg	Glu	Arg	Pro	Glu	Arg	Ile	Glu	Ala	Thr	Leu	Asp	Ser	481
Leu	Gly	Ile	Ser	Asp	Glu	Leu	Lys	Glu	Lys	Leu	Glu	Asp	494
Val	Leu	Ile	Pro	Glu	Gln	Gln	Phe	Thr	Leu	Gly	Arg	Met	507
Leu	Gly	Lys	Gly	Glu	Phe	Gly	Ser	Val	Arg	Glu	Ala	Gln	520

Leu	Lys	Gln	Glu	Asp	Gly	Ser	Phe	Val	Lys	Val	Ala	Val	533
Lys	Met	Leu	Lys	Ala	Asp	Ile	Ile	Ala	Ser	Ser	Asp	Ile	546
Glu	Glu	Phe	Leu	Arg	Glu	Ala	Ala	Cys	Met	Lys	Glu	Phe	559
Asp	His	Pro	His	Val	Ala	Lys	Leu	Val	Gly	Val	Ser	Leu	572
Arg	Ser	Arg	Ala	Lys	Gly	Arg	Leu	Pro	Ile	Pro	Met	Val	585
Ile	Leu	Pro	Phe	Met	Lys	His	Gly	Asp	Leu	His	Ala	Phe	598
Leu	Leu	Ala	Ser	Arg	Ile	Gly	Glu	Asn	Pro	Phe	Asn	Leu	611
Pro	Leu	Gln	Thr	Leu	Val	Arg	Phe	Met	Val	Asp	Ile	Ala	624
Cys	Gly	Met	Glu	Tyr	Leu	Ser	Ser	Arg	Asn	Phe	Ile	His	637
Arg	Asp	Leu	Ala	Ala	Arg	Asn	Cys	Met	Leu	Ala	Glu	Asp	650
Met	Thr	Val	Cys	Val	Ala	Asp	Phe	Gly	Leu	Ser	Arg	Lys	663
Ile	Tyr	Ser	Gly	Asp	Tyr	Tyr	Arg	Gln	Gly	Cys	Ala	Ser	676
Lys	Leu	Pro	Val	Lys	Trp	Leu	Ala	Leu	Glu	Ser	Leu	Ala	689
Asp	Asn	Leu	Tyr	Thr	Val	His	Ser	Asp	Val	Trp	Ala	Phe	702
Gly	Val	Thr	Met	Trp	Glu	Ile	Met	Thr	Arg	Gly	Gln	Thr	715
Pro	Tyr	Ala	Gly	Ile	Glu	Asn	Ala	Glu	Ile	Tyr	Asn	Tyr	728
Leu	Ile	Gly	Gly	Asn	Arg	Leu	Lys	Gln	Pro	Pro	Glu	Cys	741
Met	Glu	Glu	Val	Tyr	Asp	Leu	Met	Tyr	Gln	Cys	Trp	Ser	754
Ala	Asp	Pro	Lys	Gln	Arg	Pro	Ser	Phe	Thr	Cys	Leu	Arg	767
Met	Glu	Leu	Glu	Asn	Ile	Leu	Gly	His	Leu	Ser	Val	Leu	780
Ser	Thr	Ser	Gln	Asp	Pro	Leu	Tyr	Ile	Asn	Ile	Glu	Arg	793
Ala	Glu	Gln	Pro	Thr	Glu	Ser	Gly	Ser	Pro	Glu	Leu	His	806
Cys	Gly	Glu	Arg	Ser	Ser	Ser	Glu	Ala	Gly	Asp	Gly	Ser	819
Gly	Val	Gly	Ala	Val	Gly	Gly	Ile	Pro	Ser	Asp	Ser	Arg	832
Tyr	Ile	Phe	Ser	Pro	Gly	Gly	Leu	Ser	Glu	Ser	Pro	Gly	845
Gln	Leu	Glu	Gln	Gln	Pro	Glu	Ser	Pro	Leu	Asn	Glu	Asn	858
Gln	Arg	Leu	Leu	Leu	Leu	Gln	Gln	Gly	Leu	Leu	Pro	His	871
Ser	Ser	Cys											874

(3) INFORMATION FOR SEQUENCE ID NO. 2:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 850 AMINO ACIDS

(B) TYPE: AMINO ACID

(C) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: PROTEIN

(3) SEQUENCE DESCRIPTION: SEQ ID NO. 2:

											Ala	Gly	2
Leu	Lys	Leu	Met	Gly	Ala	Pro	Val	Lys	Met	Thr	Val	Ser	15
Gln	Gly	Gln	Pro	Val	Lys	Leu	Asn	Cys	Ser	Val	Glu	Gly	28
Met	Glu	Asp	Pro	Asp	Ile	His	Trp	Met	Lys	Asp	Gly	Thr	41
Val	Val	Gln	Asn	Ala	Ser	Gln	Val	Ser	Ile	Ser	Ile	Ser	54
Glu	His	Ser	Trp	Ile	Gly	Leu	Leu	Ser	Leu	Lys	Ser	Val	67
Glu	Arg	Ser	Asp	Ala	Gly	Leu	Tyr	Trp	Cys	Gln	Val	Lys	80
Asp	Gly	Glu	Glu	Thr	Lys	Ile	Ser	Gln	Ser	Val	Trp	Leu	93
Thr	Val	Glu	Gly	Val	Pro	Phe	Phe	Thr	Val	Glu	Pro	Lys	106
Asp	Leu	Ala	Val	Pro	Pro	Asn	Ala	Pro	Phe	Gln	Leu	Ser	119
Cys	Glu	Ala	Val	Gly	Pro	Pro	Glu	Pro	Val	Thr	Ile	Tyr	132
Trp	Trp	Arg	Gly	Leu	Thr	Lys	Val	Gly	Gly	Pro	Ala	Pro	145
Ser	Pro	Ser	Val	Leu	Asn	Val	Thr	Gly	Val	Thr	Gln	Arg	158
Thr	Glu	Phe	Ser	Cys	Glu	Ala	Arg	Asn	Ile	Lys	Gly	Leu	171
Ala	Thr	Ser	Arg	Pro	Ala	Ile	Val	Arg	Leu	Gln	Ala	Pro	184
Pro	Ala	Ala	Pro	Phe	Asn	Thr	Thr	Val	Thr	Thr	Ile	Ser	197
Ser	Tyr	Asn	Ala	Ser	Val	Ala	Trp	Val	Pro	Gly	Ala	Asp	210
Gly	Leu	Ala	Leu	Leu	His	Ser	Cys	Thr	Val	Gln	Val	Ala	223
His	Ala	Pro	Gly	Glu	Trp	Glu	Ala	Leu	Ala	Val	Val	Val	236
Pro	Val	Pro	Pro	Phe	Thr	Cys	Leu	Leu	Arg	Asn	Leu	Ala	249
Pro	Ala	Thr	Asn	Tyr	Ser	Leu	Arg	Val	Arg	Cys	Ala	Asn	262
Ala	Leu	Gly	Pro	Ser	Pro	Tyr	Gly	Asp	Trp	Val	Pro	Phe	275
Gln	Thr	Lys	Gly	Leu	Ala	Pro	Ala	Arg	Ala	Pro	Gln	Asn	288
Phe	His	Ala	Ile	Arg	Thr	Asp	Ser	Gly	Leu	Ile	Leu	Glu	301
Trp	Glu	Glu	Val	Ile	Pro	Glu	Asp	Pro	Gly	Glu	Gly	Pro	314
Leu	Gly	Pro	Tyr	Lys	Leu	Ser	Trp	Val	Gln	Glu	Asn	Gly	327
Thr	Gln	Asp	Glu	Leu	Met	Val	Glu	Gly	Thr	Arg	Ala	Asn	340
Leu	Thr	Asp	Trp	Asp	Pro	Gln	Lys	Asp	Leu	Ile	Leu	Arg	353
Val	Cys	Ala	Ser	Asn	Ala	Ile	Gly	Asp	Gly	Pro	Trp	Ser	366
Gln	Pro	Leu	Val	Val	Ser	Ser	His	Asp	His	Ala	Gly	Arg	379
Gln	Gly	Pro	Pro	His	Ser	Arg	Thr	Ser	Trp	Val	Pro	Val	392
Val	Leu	Gly	Val	Leu	Thr	Ala	Leu	Ile	Thr	Ala	Ala	Ala	405

Leu	Ala	Leu	Ile	Leu	Leu	Arg	Lys	Arg	Arg	Lys	Glu	Thr	418
Arg	Phe	Gly	Gln	Ala	Phe	Asp	Ser	Val	Met	Ala	Arg	Gly	431
Glu	Pro	Ala	Val	His	Phe	Arg	Ala	Ala	Arg	Ser	Phe	Asn	444
Arg	Glu	Arg	Pro	Glu	Arg	Ile	Glu	Ala	Thr	Leu	Asp	Ser	457
Leu	Gly	Ile	Ser	Asp	Glu	Leu	Lys	Glu	Lys	Leu	Glu	Asp	470
Val	Leu	Ile	Pro	Glu	Gln	Gln	Phe	Thr	Leu	Gly	Arg	Met	483
Leu	Gly	Lys	Gly	Glu	Phe	Gly	Ser	Val	Arg	Glu	Ala	Gln	496
Leu	Lys	Gln	Glu	Asp	Gly	Ser	Phe	Val	Lys	Val	Ala	Val	509
Lys	Met	Leu	Lys	Ala	Asp	Ile	Ile	Ala	Ser	Ser	Asp	Ile	522
Glu	Glu	Phe	Leu	Arg	Glu	Ala	Ala	Cys	Met	Lys	Glu	Phe	535
Asp	His	Pro	His	Val	Ala	Lys	Leu	Val	Gly	Val	Ser	Leu	548
Arg	Ser	Arg	Ala	Lys	Gly	Arg	Leu	Pro	Ile	Pro	Met	Val	561
Ile	Leu	Pro	Phe	Met	Lys	His	Gly	Asp	Leu	His	Ala	Phe	574
Leu	Leu	Ala	Ser	Arg	Ile	Gly	Glu	Asn	Pro	Phe	Asn	Leu	587
Pro	Leu	Gln	Thr	Leu	Val	Arg	Phe	Met	Val	Asp	Ile	Ala	600
Cys	Gly	Met	Glu	Tyr	Leu	Ser	Ser	Arg	Asn	Phe	Ile	His	613
Arg	Asp	Leu	Ala	Ala	Arg	Asn	Cys	Met	Leu	Ala	Glu	Asp	626
Met	Thr	Val	Cys	Val	Ala	Asp	Phe	Gly	Leu	Ser	Arg	Lys	639
Ile	Tyr	Ser	Gly	Asp	Tyr	Tyr	Arg	Gln	Gly	Cys	Ala	Ser	652
Lys	Leu	Pro	Val	Lys	Trp	Leu	Ala	Leu	Glu	Ser	Leu	Ala	665
Asp	Asn	Leu	Tyr	Thr	Val	His	Ser	Asp	Val	Trp	Ala	Phe	678
Gly	Val	Thr	Met	Trp	Glu	Ile	Met	Thr	Arg	Gly	Gln	Thr	691
Pro	Tyr	Ala	Gly	Ile	Glu	Asn	Ala	Glu	Ile	Tyr	Asn	Tyr	704
Leu	Ile	Gly	Gly	Asn	Arg	Leu	Lys	Gln	Pro	Pro	Glu	Cys	717
Met	Glu	Glu	Val	Tyr	Asp	Leu	Met	Tyr	Gln	Cys	Trp	Ser	730
Ala	Asp	Pro	Lys	Gln	Arg	Pro	Ser	Phe	Thr	Cys	Leu	Arg	743
Met	Glu	Leu	Glu	Asn	Ile	Leu	Gly	His	Leu	Ser	Val	Leu	756
Ser	Thr	Ser	Gln	Asp	Pro	Leu	Tyr	Ile	Asn	Ile	Glu	Arg	769
Ala	Glu	Gln	Pro	Thr	Glu	Ser	Gly	Ser	Pro	Glu	Leu	His	782
Cys	Gly	Glu	Arg	Ser	Ser	Ser	Glu	Ala	Gly	Asp	Gly	Ser	795
Gly	Val	Gly	Ala	Val	Gly	Gly	Ile	Pro	Ser	Asp	Ser	Arg	808
Tyr	Ile	Phe	Ser	Pro	Gly	Gly	Leu	Ser	Glu	Ser	Pro	Gly	821
Gln	Leu	Glu	Gln	Gln	Pro	Glu	Ser	Pro	Leu	Asn	Glu	Asn	834
Gln	Arg	Leu	Leu	Leu	Leu	Gln	Gln	Gly	Leu	Leu	Pro	His	847

Ser Ser Cys

850

(4) INFORMATION FOR SEQUENCE ID NO. 3:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 876 AMINO ACIDS

(B) TYPE: AMINO ACID

(C) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: PROTEIN

(3) SEQUENCE DESCRIPTION: SEQ ID NO. 3:

Met	Gly	Arg	Pro	Gly	Leu	Pro	Pro	Leu	Pro	Leu	Pro	Pro	13
Pro	Pro	Arg	Leu	Gly	Leu	Leu	Leu	Ala	Glu	Ser	Ala	Ala	26
Ala	Gly	Leu	Lys	Leu	Met	Gly	Ala	Pro	Val	Lys	Leu	Thr	39
Val	Ser	Gln	Gly	Gln	Pro	Val	Lys	Leu	Asn	Cys	Ser	Val	52
Glu	Gly	Met	Glu	Glu	Pro	Asp	Ile	Gln	Trp	Val	Lys	Asp	65
Gly	Ala	Val	Val	Gln	Asn	Leu	Asp	Gln	Leu	Tyr	Ile	Pro	78
Val	Ser	Glu	Gln	His	Trp	Ile	Gly	Phe	Leu	Ser	Leu	Lys	91
Ser	Val	Glu	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Trp	Cys	Gln	104
Val	Glu	Asp	Gly	Gly	Glu	Thr	Glu	Ile	Ser	Gln	Pro	Val	117
Trp	Leu	Thr	Val	Glu	Gly	Val	Pro	Phe	Phe	Thr	Val	Glu	130
Pro	Lys	Asp	Leu	Ala	Val	Pro	Pro	Asn	Ala	Pro	Phe	Gln	143
Leu	Ser	Cys	Glu	Ala	Val	Gly	Pro	Pro	Glu	Pro	Val	Thr	156
Ile	Val	Trp	Trp	Arg	Gly	Thr	Thr	Lys	Ile	Gly	Gly	Pro	169
Ala	Pro	Ser	Pro	Ser	Val	Leu	Asn	Val	Thr	Gly	Val	Thr	182
Gln	Ser	Thr	Met	Phe	Ser	Cys	Glu	Ala	His	Asn	Leu	Lys	195
Gly	Leu	Ala	Ser	Ser	Arg	Thr	Ala	Thr	Val	His	Leu	Gln	208
Ala	Leu	Pro	Ala	Ala	Pro	Phe	Asn	Ile	Thr	Val	Thr	Lys	221
Leu	Ser	Ser	Ser	Asn	Ala	Ser	Val	Ala	Trp	Met	Pro	Gly	234
Ala	Asp	Gly	Arg	Ala	Leu	Leu	Gln	Ser	Cys	Thr	Val	Gln	247
Val	Thr	Gln	Ala	Pro	Gly	Gly	Trp	Glu	Val	Leu	Ala	Val	260
Val	Val	Pro	Val	Pro	Pro	Phe	Thr	Cys	Leu	Leu	Arg	Asp	273
Leu	Val	Pro	Ala	Thr	Asn	Tyr	Ser	Leu	Arg	Val	Arg	Cys	286
Ala	Asn	Ala	Leu	Gly	Pro	Ser	Pro	Tyr	Ala	Asp	Trp	Val	299
Pro	Phe	Gln	Thr	Lys	Gly	Leu	Ala	Pro	Ala	Ser	Ala	Pro	312
Gln	Asn	Leu	His	Ala	Ile	Arg	Thr	Asp	Ser	Gly	Leu	Ile	325

Leu	Glu	Trp	Glu	Glu	Val	Ile	Pro	Glu	Ala	Pro	Leu	Glu	338
Gly	Pro	Leu	Gly	Pro	Tyr	Lys	Leu	Ser	Trp	Val	Gln	Asp	351
Asn	Gly	Thr	Gln	Asp	Glu	Leu	Thr	Val	Glu	Gly	Thr	Arg	364
Ala	Asn	Leu	Thr	Gly	Trp	Asp	Pro	Gln	Lys	Asp	Leu	Ile	377
Val	Arg	Val	Cys	Val	Ser	Asn	Ala	Val	Gly	Cys	Gly	Pro	390
Trp	Ser	Gln	Pro	Leu	Val	Val	Ser	Ser	His	Asp	Arg	Ala	403
Gly	Gln	Gln	Gly	Pro	Pro	His	Ser	Arg	Thr	Ser	Trp	Val	416
Pro	Val	Val	Leu	Gly	Val	Leu	Thr	Ala	Leu	Val	Thr	Ala	429
Ala	Ala	Leu	Ala	Leu	Ile	Leu	Leu	Arg	Lys	Arg	Arg	Lys	442
Glu	Thr	Arg	Phe	Gly	Gln	Ala	Phe	Asp	Ser	Val	Met	Ala	455
Arg	Gly	Glu	Pro	Ala	Val	His	Phe	Arg	Ala	Ala	Arg	Ser	468
Phe	Asn	Arg	Glu	Arg	Pro	Glu	Arg	Ile	Glu	Ala	Thr	Leu	481
Asp	Ser	Leu	Gly	Ile	Ser	Asp	Glu	Leu	Lys	Glu	Lys	Leu	494
Glu	Asp	Val	Leu	Ile	Pro	Glu	Gln	Gln	Phe	Thr	Leu	Gly	507
Arg	Met	Leu	Gly	Lys	Gly	Glu	Phe	Gly	Ser	Val	Arg	Glu	520
Ala	Gln	Leu	Lys	Gln	Glu	Asp	Gly	Ser	Phe	Val	Lys	Val	533
Ala	Val	Lys	Met	Leu	Lys	Ala	Asp	Ile	Ile	Ala	Ser	Ser	546
Asp	Ile	Glu	Glu	Phe	Leu	Arg	Glu	Ala	Ala	Cys	Met	Lys	559
Glu	Phe	Asp	His	Pro	His	Val	Ala	Lys	Leu	Val	Gly	Val	572
Ser	Leu	Arg	Ser	Arg	Ala	Lys	Gly	Arg	Leu	Pro	Ile	Pro	585
Met	Val	Ile	Leu	Pro	Phe	Met	Lys	His	Gly	Asp	Leu	His	598
Ala	Phe	Leu	Leu	Ala	Ser	Arg	Ile	Gly	Glu	Asn	Pro	Phe	611
Asn	Leu	Pro	Leu	Gln	Thr	Leu	Ile	Arg	Phe	Met	Val	Asp	624
Ile	Ala	Cys	Gly	Met	Glu	Tyr	Leu	Ser	Ser	Arg	Asn	Phe	637
Ile	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Cys	Met	Leu	Ala	650
Glu	Asp	Met	Thr	Val	Cys	Val	Ala	Asp	Phe	Gly	Leu	Ser	663
Arg	Lys	Ile	Tyr	Ser	Gly	Asp	Tyr	Tyr	Arg	Gln	Gly	Cys	676
Ala	Ser	Lys	Leu	Pro	Val	Lys	Trp	Leu	Ala	Leu	Glu	Ser	689
Leu	Ala	Asp	Asn	Leu	Tyr	Thr	Val	Gln	Ser	Asp	Val	Trp	702
Ala	Phe	Gly	Val	Thr	Met	Trp	Glu	Ile	Met	Thr	Arg	Gly	715
Gln	Thr	Pro	Tyr	Ala	Gly	Ile	Glu	Asn	Ala	Glu	Ile	Tyr	728
Asn	Tyr	Leu	Ile	Gly	Gly	Asn	Arg	Leu	Lys	Gln	Pro	Pro	741
Glu	Cys	Met	Glu	Asp	Val	Tyr	Asp	Leu	Met	Tyr	Gln	Cys	754
Trp	Ser	Ala	Asp	Pro	Lys	Gln	Arg	Pro	Ser	Phe	Thr	Cys	767

Leu	Arg	Met	Glu	Leu	Glu	Asn	Ile	Leu	Gly	Gln	Leu	Ser	780
Val	Leu	Ser	Ala	Ser	Gln	Asp	Pro	Leu	Tyr	Ile	Asn	Ile	793
Glu	Arg	Ala	Glu	Glu	Pro	Thr	Val	Gly	Gly	Ser	Leu	Glu	806
Leu	Pro	Gly	Arg	Asp	Gln	Pro	Tyr	Ser	Gly	Ala	Gly	Asp	819
Gly	Ser	Gly	Met	Gly	Ala	Val	Gly	Gly	Thr	Pro	Ser	Asp	832
Cys	Arg	Tyr	Ile	Leu	Thr	Pro	Gly	Gly	Leu	Ala	Glu	Gln	845
Pro	Gly	Gln	Ala	Glu	His	Gln	Pro	Glu	Ser	Pro	Leu	Asn	858
Glu	Thr	Gln	Arg	Leu	Leu	Leu	Leu	Gln	Gln	Gly	Leu	Leu	871
Pro	His	Ser	Ser	Cys									876

(5) INFORMATION FOR SEQUENCE ID NO. 4:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 850 AMINO ACIDS

(B) TYPE: AMINO ACID

(C) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: PROTEIN

(3) SEQUENCE DESCRIPTION: SEQ ID NO. 4:

Ala	Gly	Leu	Lys	Leu	Met	Gly	Ala	Pro	Val	Lys	Leu	Thr	13
Val	Ser	Gln	Gly	Gln	Pro	Val	Lys	Leu	Asn	Cys	Ser	Val	26
Glu	Gly	Met	Glu	Glu	Pro	Asp	Ile	Gln	Trp	Val	Lys	Asp	39
Gly	Ala	Val	Val	Gln	Asn	Leu	Asp	Gln	Leu	Tyr	Ile	Pro	52
Val	Ser	Glu	Gln	His	Trp	Ile	Gly	Phe	Leu	Ser	Leu	Lys	65
Ser	Val	Glu	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Trp	Cys	Gln	78
Val	Glu	Asp	Gly	Gly	Glu	Thr	Glu	Ile	Ser	Gln	Pro	Val	91
Trp	Leu	Thr	Val	Glu	Gly	Val	Pro	Phe	Phe	Thr	Val	Glu	104
Pro	Lys	Asp	Leu	Ala	Val	Pro	Pro	Asn	Ala	Pro	Phe	Gln	117
Leu	Ser	Cys	Glu	Ala	Val	Gly	Pro	Pro	Glu	Pro	Val	Thr	130
Ile	Val	Trp	Trp	Arg	Gly	Thr	Thr	Lys	Ile	Gly	Gly	Pro	143
Ala	Pro	Ser	Pro	Ser	Val	Leu	Asn	Val	Thr	Gly	Val	Thr	156
Gln	Ser	Thr	Met	Phe	Ser	Cys	Glu	Ala	His	Asn	Leu	Lys	169
Gly	Leu	Ala	Ser	Ser	Arg	Thr	Ala	Thr	Val	His	Leu	Gln	182
Ala	Leu	Pro	Ala	Ala	Pro	Phe	Asn	Ile	Thr	Val	Thr	Lys	195
Leu	Ser	Ser	Ser	Asn	Ala	Ser	Val	Ala	Trp	Met	Pro	Gly	208
Ala	Asp	Gly	Arg	Ala	Leu	Leu	Gln	Ser	Cys	Thr	Val	Gln	221
Val	Thr	Gln	Ala	Pro	Gly	Gly	Trp	Glu	Val	Leu	Ala	Val	234

Val	Val	Pro	Val	Pro	Pro	Phe	Thr	Cys	Leu	Leu	Arg	Asp	247
Leu	Val	Pro	Ala	Thr	Asn	Tyr	Ser	Leu	Arg	Val	Arg	Cys	260
Ala	Asn	Ala	Leu	Gly	Pro	Ser	Pro	Tyr	Ala	Asp	Trp	Val	273
Pro	Phe	Gln	Thr	Lys	Gly	Leu	Ala	Pro	Ala	Ser	Ala	Pro	286
Gln	Asn	Leu	His	Ala	Ile	Arg	Thr	Asp	Ser	Gly	Leu	Ile	299
Leu	Glu	Trp	Glu	Glu	Val	Ile	Pro	Glu	Ala	Pro	Leu	Glu	312
Gly	Pro	Leu	Gly	Pro	Tyr	Lys	Leu	Ser	Trp	Val	Gln	Asp	325
Asn	Gly	Thr	Gln	Asp	Glu	Leu	Thr	Val	Glu	Gly	Thr	Arg	338
Ala	Asn	Leu	Thr	Gly	Trp	Asp	Pro	Gln	Lys	Asp	Leu	Ile	351
Val	Arg	Val	Cys	Val	Ser	Asn	Ala	Val	Gly	Cys	Gly	Pro	364
Trp	Ser	Gln	Pro	Leu	Val	Val	Ser	Ser	His	Asp	Arg	Ala	377
Gly	Gln	Gln	Gly	Pro	Pro	His	Ser	Arg	Thr	Ser	Trp	Val	390
Pro	Val	Val	Leu	Gly	Val	Leu	Thr	Ala	Leu	Val	Thr	Ala	403
Ala	Ala	Leu	Ala	Leu	Ile	Leu	Leu	Arg	Lys	Arg	Arg	Lys	416
Glu	Thr	Arg	Phe	Gly	Gln	Ala	Phe	Asp	Ser	Val	Met	Ala	429
Arg	Gly	Glu	Pro	Ala	Val	His	Phe	Arg	Ala	Ala	Arg	Ser	442
Phe	Asn	Arg	Glu	Arg	Pro	Glu	Arg	Ile	Glu	Ala	Thr	Leu	455
Asp	Ser	Leu	Gly	Ile	Ser	Asp	Glu	Leu	Lys	Glu	Lys	Leu	468
Glu	Asp	Val	Leu	Ile	Pro	Glu	Gln	Gln	Phe	Thr	Leu	Gly	481
Arg	Met	Leu	Gly	Lys	Gly	Glu	Phe	Gly	Ser	Val	Arg	Glu	494
Ala	Gln	Leu	Lys	Gln	Glu	Asp	Gly	Ser	Phe	Val	Lys	Val	507
Ala	Val	Lys	Met	Leu	Lys	Ala	Asp	Ile	Ile	Ala	Ser	Ser	520
Asp	Ile	Glu	Glu	Phe	Leu	Arg	Glu	Ala	Ala	Cys	Met	Lys	533
Glu	Phe	Asp	His	Pro	His	Val	Ala	Lys	Leu	Val	Gly	Val	546
Ser	Leu	Arg	Ser	Arg	Ala	Lys	Gly	Arg	Leu	Pro	Ile	Pro	559
Met	Val	Ile	Leu	Pro	Phe	Met	Lys	His	Gly	Asp	Leu	His	572
Ala	Phe	Leu	Leu	Ala	Ser	Arg	Ile	Gly	Glu	Asn	Pro	Phe	585
Asn	Leu	Pro	Leu	Gln	Thr	Leu	Ile	Arg	Phe	Met	Val	Asp	598
Ile	Ala	Cys	Gly	Met	Glu	Tyr	Leu	Ser	Ser	Arg	Asn	Phe	611
Ile	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Cys	Met	Leu	Ala	624
Glu	Asp	Met	Thr	Val	Cys	Val	Ala	Asp	Phe	Gly	Leu	Ser	637
Arg	Lys	Ile	Tyr	Ser	Gly	Asp	Tyr	Tyr	Arg	Gln	Gly	Cys	650
Ala	Ser	Lys	Leu	Pro	Val	Lys	Trp	Leu	Ala	Leu	Glu	Ser	663
Leu	Ala	Asp	Asn	Leu	Tyr	Thr	Val	Gln	Ser	Asp	Val	Trp	676

Ala	Phe	Gly	Val	Thr	Met	Trp	Glu	Ile	Met	Thr	Arg	Gly	689
Gln	Thr	Pro	Tyr	Ala	Gly	Ile	Glu	Asn	Ala	Glu	Ile	Tyr	702
Asn	Tyr	Leu	Ile	Gly	Gly	Asn	Arg	Leu	Lys	Gln	Pro	Pro	715
Glu	Cys	Met	Glu	Asp	Val	Tyr	Asp	Leu	Met	Tyr	Gln	Cys	728
Trp	Ser	Ala	Asp	Pro	Lys	Gln	Arg	Pro	Ser	Phe	Thr	Cys	741
Leu	Arg	Met	Glu	Leu	Glu	Asn	Ile	Leu	Gly	Gln	Leu	Ser	754
Val	Leu	Ser	Ala	Ser	Gln	Asp	Pro	Leu	Tyr	Ile	Asn	Ile	767
Glu	Arg	Ala	Glu	Glu	Pro	Thr	Val	Gly	Gly	Ser	Leu	Glu	780
Leu	Pro	Gly	Arg	Asp	Gln	Pro	Tyr	Ser	Gly	Ala	Gly	Asp	793
Gly	Ser	Gly	Met	Gly	Ala	Val	Gly	Gly	Thr	Pro	Ser	Asp	806
Cys	Arg	Tyr	Ile	Leu	Thr	Pro	Gly	Gly	Leu	Ala	Glu	Gln	819
Pro	Gly	Gln	Ala	Glu	His	Gln	Pro	Glu	Ser	Pro	Leu	Asn	832
Glu	Thr	Gln	Arg	Leu	Leu	Leu	Leu	Gln	Gln	Gly	Leu	Leu	845
Pro	His	Ser	Ser	Cys									850

(6) INFORMATION FOR SEQUENCE ID NO. 5:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 386 AMINO ACIDS

(B) TYPE: AMINO ACID

(C) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: PROTEIN

(3) SEQUENCE DESCRIPTION: SEQ ID NO. 5:

											Ala	Gly	2
Leu	Lys	Leu	Met	Gly	Ala	Pro	Val	Lys	Met	Thr	Val	Ser	15
Gln	Gly	Gln	Pro	Val	Lys	Leu	Asn	Cys	Ser	Val	Glu	Gly	28
Met	Glu	Asp	Pro	Asp	Ile	His	Trp	Met	Lys	Asp	Gly	Thr	41
Val	Val	Gln	Asn	Ala	Ser	Gln	Val	Ser	Ile	Ser	Ile	Ser	54
Glu	His	Ser	Trp	Ile	Gly	Leu	Leu	Ser	Leu	Lys	Ser	Val	67
Glu	Arg	Ser	Asp	Ala	Gly	Leu	Tyr	Trp	Cys	Gln	Val	Lys	80
Asp	Gly	Glu	Glu	Thr	Lys	Ile	Ser	Gln	Ser	Val	Trp	Leu	93
Thr	Val	Glu	Gly	Val	Pro	Phe	Phe	Thr	Val	Glu	Pro	Lys	106
Asp	Leu	Ala	Val	Pro	Pro	Asn	Ala	Pro	Phe	Gln	Leu	Ser	119
Cys	Glu	Ala	Val	Gly	Pro	Pro	Glu	Pro	Val	Thr	Ile	Tyr	132
Trp	Trp	Arg	Gly	Leu	Thr	Lys	Val	Gly	Gly	Pro	Ala	Pro	145
Ser	Pro	Ser	Val	Leu	Asn	Val	Thr	Gly	Val	Thr	Gln	Arg	158

Thr	Glu	Phe	Ser	Cys	Glu	Ala	Arg	Asn	Ile	Lys	Gly	Leu	171
Ala	Thr	Ser	Arg	Pro	Ala	Ile	Val	Arg	Leu	Gln	Ala	Pro	184
Pro	Ala	Ala	Pro	Phe	Asn	Thr	Thr	Val	Thr	Thr	Ile	Ser	197
Ser	Tyr	Asn	Ala	Ser	Val	Ala	Trp	Val	Pro	Gly	Ala	Asp	210
Gly	Leu	Ala	Leu	Leu	His	Ser	Cys	Thr	Val	Gln	Val	Ala	223
His	Ala	Pro	Gly	Glu	Trp	Glu	Ala	Leu	Ala	Val	Val	Val	236
Pro	Val	Pro	Pro	Phe	Thr	Cys	Leu	Leu	Arg	Asn	Leu	Ala	249
Pro	Ala	Thr	Asn	Tyr	Ser	Leu	Arg	Val	Arg	Cys	Ala	Asn	262
Ala	Leu	Gly	Pro	Ser	Pro	Tyr	Gly	Asp	Trp	Val	Pro	Phe	275
Gln	Thr	Lys	Gly	Leu	Ala	Pro	Ala	Arg	Ala	Pro	Gln	Asn	288
Phe	His	Ala	Ile	Arg	Thr	Asp	Ser	Gly	Leu	Ile	Leu	Glu	301
Trp	Glu	Glu	Val	Ile	Pro	Glu	Asp	Pro	Gly	Glu	Gly	Pro	314
Leu	Gly	Pro	Tyr	Lys	Leu	Ser	Trp	Val	Gln	Glu	Asn	Gly	327
Thr	Gln	Asp	Glu	Leu	Met	Val	Glu	Gly	Thr	Arg	Ala	Asn	340
Leu	Thr	Asp	Trp	Asp	Pro	Gln	Lys	Asp	Leu	Ile	Leu	Arg	353
Val	Cys	Ala	Ser	Asn	Ala	Ile	Gly	Asp	Gly	Pro	Trp	Ser	366
Gln	Pro	Leu	Val	Val	Ser	Ser	His	Asp	His	Ala	Gly	Arg	379
Gln	Gly	Pro	Pro	His	Ser	Arg							386

(7) INFORMATION FOR SEQUENCE ID NO. 6:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 386 AMINO ACIDS

(B) TYPE: AMINO ACID

(C) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: PROTEIN

(3) SEQUENCE DESCRIPTION: SEQ ID NO. 6:

Ala	Gly	Leu	Lys	Leu	Met	Gly	Ala	Pro	Val	Lys	Leu	Thr	13
Val	Ser	Gln	Gly	Gln	Pro	Val	Lys	Leu	Asn	Cys	Ser	Val	26
Glu	Gly	Met	Glu	Glu	Pro	Asp	Ile	Gln	Trp	Val	Lys	Asp	39
Gly	Ala	Val	Val	Gln	Asn	Leu	Asp	Gln	Leu	Tyr	Ile	Pro	52
Val	Ser	Glu	Gln	His	Trp	Ile	Gly	Phe	Leu	Ser	Leu	Lys	65
Ser	Val	Glu	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Trp	Cys	Gln	78
Val	Glu	Asp	Gly	Gly	Glu	Thr	Glu	Ile	Ser	Gln	Pro	Val	91
Trp	Leu	Thr	Val	Glu	Gly	Val	Pro	Phe	Phe	Thr	Val	Glu	104
Pro	Lys	Asp	Leu	Ala	Val	Pro	Pro	Asn	Ala	Pro	Phe	Gln	117

Leu	Ser	Cys	Glu	Ala	Val	Gly	Pro	Pro	Glu	Pro	Val	Thr	130
Ile	Val	Trp	Trp	Arg	Gly	Thr	Thr	Lys	Ile	Gly	Gly	Pro	143
Ala	Pro	Ser	Pro	Ser	Val	Leu	Asn	Val	Thr	Gly	Val	Thr	156
Gln	Ser	Thr	Met	Phe	Ser	Cys	Glu	Ala	His	Asn	Leu	Lys	169
Gly	Leu	Ala	Ser	Ser	Arg	Thr	Ala	Thr	Val	His	Leu	Gln	182
Ala	Leu	Pro	Ala	Ala	Pro	Phe	Asn	Ile	Thr	Val	Thr	Lys	195
Leu	Ser	Ser	Ser	Asn	Ala	Ser	Val	Ala	Trp	Met	Pro	Gly	208
Ala	Asp	Gly	Arg	Ala	Leu	Leu	Gln	Ser	Cys	Thr	Val	Gln	221
Val	Thr	Gln	Ala	Pro	Gly	Gly	Trp	Glu	Val	Leu	Ala	Val	234
Val	Val	Pro	Val	Pro	Pro	Phe	Thr	Cys	Leu	Leu	Arg	Asp	247
Leu	Val	Pro	Ala	Thr	Asn	Tyr	Ser	Leu	Arg	Val	Arg	Cys	260
Ala	Asn	Ala	Leu	Gly	Pro	Ser	Pro	Tyr	Ala	Asp	Trp	Val	273
Pro	Phe	Gln	Thr	Lys	Gly	Leu	Ala	Pro	Ala	Ser	Ala	Pro	286
Gln	Asn	Leu	His	Ala	Ile	Arg	Thr	Asp	Ser	Gly	Leu	Ile	299
Leu	Glu	Trp	Glu	Glu	Val	Ile	Pro	Glu	Ala	Pro	Leu	Glu	312
Gly	Pro	Leu	Gly	Pro	Tyr	Lys	Leu	Ser	Trp	Val	Gln	Asp	325
Asn	Gly	Thr	Gln	Asp	Glu	Leu	Thr	Val	Glu	Gly	Thr	Arg	338
Ala	Asn	Leu	Thr	Gly	Trp	Asp	Pro	Gln	Lys	Asp	Leu	Ile	351
Val	Arg	Val	Cys	Val	Ser	Asn	Ala	Val	Gly	Cys	Gly	Pro	364
Trp	Ser	Gln	Pro	Leu	Val	Val	Ser	Ser	His	Asp	Arg	Ala	377
Gly	Gln	Gln	Gly	Pro	Pro	His	Ser	Arg					386

(8) INFORMATION FOR SEQUENCE ID NO. 7:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3919 BASE PAIRS

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: cDNA

(3) SEQUENCE DESCRIPTION: SEQ ID NO. 7:

GGC	CAC	GAG	TGT	GGA	AGG	AGC	GCG	GTT	GG	CCC	CAG	CCG	CAG	CCCC	GGG	ACT	CCT	CGT	GCT	G	60
ACG	GCG	GTG	GCG	CGG	GCT	CTA	GGC	GGC	CGG	CGG	TCCC	GG	ACG	CCCC	GGC	CGG	AGC	CGC	CGC	C	120
CCCC	CCCC	TCC	CGC	GGG	CCT	CCCC	CCCC	TCT	CCG	CC	ACC	CTC	CTC	CAG	CGC	T	CGC	CGG		180	
GCC	GGG	CCCC	GGC	ATG	GTG	CGG	CGT	CGC	CGG	ATG	GGC	GCT	GAG	GGC	GAG					230	

Met	Gly	Trp	Pro	Gly	Leu	Arg	Pro	Leu	Leu	Leu	Ala	Gly	
ATG	GGG	TGG	CCG	GGG	CTC	CGG	CCG	CTG	CTG	CTG	GCG	GGA	269

Leu	Ala	Ser	Leu	Leu	Leu	Pro	Gly	Ser	Ala	Ala	Ala	Gly	308
CTG	GCT	TCT	CTG	CTG	CTC	CCC	GGG	TCT	GCG	GCC	GCA	GGC	
Leu	Lys	Leu	Met	Gly	Ala	Pro	Val	Lys	Met	Thr	Val	Ser	347
CTG	AAG	CTC	ATG	GGC	GCC	CCA	GTG	AAG	ATG	ACC	GTG	TCT	
Gln	Gly	Gln	Pro	Val	Lys	Leu	Asn	Cys	Ser	Val	Glu	Gly	386
CAG	GGG	CAG	CCA	GTG	AAG	CTC	AAC	TGC	AGC	GTG	GAG	GGG	
Met	Glu	Asp	Pro	Asp	Ile	His	Trp	Met	Lys	Asp	Gly	Thr	425
ATG	GAG	GAC	CCT	GAC	ATC	CAC	TGG	ATG	AAG	GAT	GGC	ACC	
Val	Val	Gln	Asn	Ala	Ser	Gln	Val	Ser	Ile	Ser	Ile	Ser	464
GTG	GTC	CAG	AAT	GCA	AGC	CAG	GTG	TCC	ATC	TCC	ATC	AGC	
Glu	His	Ser	Trp	Ile	Gly	Leu	Leu	Ser	Leu	Lys	Ser	Val	503
GAG	CAC	AGC	TGG	ATT	GGC	TTA	CTC	AGC	CTA	AAG	TCA	GTG	
Glu	Arg	Ser	Asp	Ala	Gly	Leu	Tyr	Trp	Cys	Gln	Val	Lys	542
GAG	CGG	TCT	GAT	GCT	GGC	CTG	TAC	TGG	TGC	CAG	GTG	AAG	
Asp	Gly	Glu	Glu	Thr	Lys	Ile	Ser	Gln	Ser	Val	Trp	Leu	581
GAT	GGG	GAG	GAA	ACC	AAG	ATC	TCT	CAG	TCA	GTA	TGG	CTC	
Thr	Val	Glu	Gly	Val	Pro	Phe	Phe	Thr	Val	Glu	Pro	Lys	620
ACT	GTC	GAA	GGT	GTG	CCA	TTC	TTC	ACA	GTG	GAA	CCA	AAA	
Asp	Leu	Ala	Val	Pro	Pro	Asn	Ala	Pro	Phe	Gln	Leu	Ser	659
GAT	CTG	GCG	GTG	CCA	CCC	AAT	GCC	CCT	TTT	CAG	CTG	TCT	
Cys	Glu	Ala	Val	Gly	Pro	Pro	Glu	Pro	Val	Thr	Ile	Tyr	698
TGT	GAG	GCT	GTG	GGT	CCT	CCA	GAA	CCC	GTA	ACC	ATT	TAC	
Trp	Trp	Arg	Gly	Leu	Thr	Lys	Val	Gly	Gly	Pro	Ala	Pro	737
TGG	TGG	AGA	GGA	CTC	ACT	AAA	GTT	GGG	GGA	CCT	GCT	CCC	
Ser	Pro	Ser	Val	Leu	Asn	Val	Thr	Gly	Val	Thr	Gln	Arg	776
TCT	CCC	TCT	GTT	TTA	AAT	GTG	ACA	GGA	GTG	ACC	CAG	CGC	
Thr	Glu	Phe	Ser	Cys	Glu	Ala	Arg	Asn	Ile	Lys	Gly	Leu	815
ACA	GAG	TTT	TCT	TGT	GAA	GCC	CGC	AAC	ATA	AAA	GGC	CTG	
Ala	Thr	Ser	Arg	Pro	Ala	Ile	Val	Arg	Leu	Gln	Ala	Pro	854
GCC	ACT	TCC	CGA	CCA	GCC	ATT	GTT	CGC	CTT	CAA	GCA	CCG	
Pro	Ala	Ala	Pro	Phe	Asn	Thr	Thr	Val	Thr	Thr	Ile	Ser	893
CCT	GCA	GCT	CCT	TTC	AAC	ACC	ACA	GTA	ACA	ACG	ATC	TCC	
Ser	Tyr	Asn	Ala	Ser	Val	Ala	Trp	Val	Pro	Gly	Ala	Asp	932
AGC	TAC	AAC	GCT	AGC	GTG	GCC	TGG	GTG	CCA	GGT	GCT	GAC	
Gly	Leu	Ala	Leu	Leu	His	Ser	Cys	Thr	Val	Gln	Val	Ala	971
GGC	CTA	GCT	CTG	CTG	CAT	TCC	TGT	ACT	GTA	CAG	GTG	GCA	
His	Ala	Pro	Gly	Glu	Trp	Glu	Ala	Leu	Ala	Val	Val	Val	1010
CAC	GCC	CCA	GGA	GAA	TGG	GAG	GCC	CTT	GCT	GTT	GTG	GTT	
Pro	Val	Pro	Pro	Phe	Thr	Cys	Leu	Leu	Arg	Asn	Leu	Ala	1049
CCT	GTG	CCA	CCT	TTT	ACC	TGC	CTG	CTT	CGG	AAC	TTG	GCC	
Pro	Ala	Thr	Asn	Tyr	Ser	Leu	Arg	Val	Arg	Cys	Ala	Asn	1088
CCT	GCC	ACC	AAC	TAC	AGC	CTT	AGG	GTG	CGC	TGT	GCC	AAT	
Ala	Leu	Gly	Pro	Ser	Pro	Tyr	Gly	Asp	Trp	Val	Pro	Phe	1127
GCC	TTG	GGC	CCT	TCT	CCC	TAC	GGC	GAC	TGG	GTG	CCC	TTT	
Gln	Thr	Lys	Gly	Leu	Ala	Pro	Ala	Arg	Ala	Pro	Gln	Asn	1166
CAG	ACA	AAG	GGC	CTA	GCG	CCA	GCC	AGA	GCT	CCT	CAG	AAT	

Phe	His	Ala	Ile	Arg	Thr	Asp	Ser	Gly	Leu	Ile	Leu	Glu	1205
TTC	CAT	GCC	ATT	CGT	ACC	GAC	TCA	GGC	CTT	ATC	CTG	GAA	
Trp	Glu	Glu	Val	Ile	Pro	Glu	Asp	Pro	Gly	Glu	Gly	Pro	1244
TGG	GAA	GAA	GTG	ATT	CCT	GAG	GAC	CCT	GGG	GAA	GGC	CCC	
Leu	Gly	Pro	Tyr	Lys	Leu	Ser	Trp	Val	Gln	Glu	Asn	Gly	1283
CTA	GGA	CCT	TAT	AAG	CTG	TCC	TGG	GTC	CAA	GAA	AAT	GGA	
Thr	Gln	Asp	Glu	Leu	Met	Val	Glu	Gly	Thr	Arg	Ala	Asn	1322
ACC	CAG	GAT	GAG	CTG	ATG	GTG	GAA	GGG	ACC	AGG	GCC	AAT	
Leu	Thr	Asp	Trp	Asp	Pro	Gln	Lys	Asp	Leu	Ile	Leu	Arg	1361
CTG	ACC	GAC	TGG	GAT	CCC	CAG	AAG	GAC	CTG	ATT	TTG	CGT	
Val	Cys	Ala	Ser	Asn	Ala	Ile	Gly	Asp	Gly	Pro	Trp	Ser	1400
GTG	TGT	GCC	TCC	AAT	GCA	ATT	GGT	GAT	GGG	CCC	TGG	AGT	
Gln	Pro	Leu	Val	Val	Ser	Ser	His	Asp	His	Ala	Gly	Arg	1439
CAG	CCA	CTG	GTG	GTG	TCT	TCT	CAT	GAC	CAT	GCA	GGG	AGG	
Gln	Gly	Pro	Pro	His	Ser	Arg	Thr	Ser	Trp	Val	Pro	Val	1478
CAG	GGC	CCT	CCC	CAC	AGC	CGC	ACA	TCC	TGG	GTG	CCT	GTG	
Val	Leu	Gly	Val	Leu	Thr	Ala	Leu	Ile	Thr	Ala	Ala	Ala	1517
GTG	CTG	GGC	GTG	CTC	ACC	GCC	CTG	ATC	ACA	GCT	GCT	GCC	
Leu	Ala	Leu	Ile	Leu	Leu	Arg	Lys	Arg	Arg	Lys	Glu	Thr	1556
TTG	GCC	CTC	ATC	CTG	CTT	CGG	AAG	AGA	CGC	AAG	GAG	ACG	
Arg	Phe	Gly	Gln	Ala	Phe	Asp	Ser	Val	Met	Ala	Arg	Gly	1595
CGT	TTC	GGG	CAA	GCC	TTT	GAC	AGT	GTC	ATG	GCC	CGA	GGG	
Glu	Pro	Ala	Val	His	Phe	Arg	Ala	Ala	Arg	Ser	Phe	Asn	1634
GAG	CCA	GCT	GTA	CAC	TTC	CGG	GCA	GCC	CGA	TCT	TTC	AAT	
Arg	Glu	Arg	Pro	Glu	Arg	Ile	Glu	Ala	Thr	Leu	Asp	Ser	1673
CGA	GAA	AGG	CCT	GAA	CGC	ATT	GAG	GCC	ACA	TTG	GAT	AGC	
Leu	Gly	Ile	Ser	Asp	Glu	Leu	Lys	Glu	Lys	Leu	Glu	Asp	1712
CTG	GGC	ATC	AGC	GAT	GAA	TTG	AAG	GAA	AAG	CTG	GAG	GAT	
Val	Leu	Ile	Pro	Glu	Gln	Gln	Phe	Thr	Leu	Gly	Arg	Met	1751
GTG	CTC	ATT	CCA	GAG	CAG	CAG	TTC	ACC	CTC	GGT	CGG	ATG	
Leu	Gly	Lys	Gly	Glu	Phe	Gly	Ser	Val	Arg	Glu	Ala	Gln	1790
TTG	GGC	AAA	GGA	GAG	TTT	GGA	TCA	GTG	CGG	GAA	GCC	CAG	
Leu	Lys	Gln	Glu	Asp	Gly	Ser	Phe	Val	Lys	Val	Ala	Val	1829
CTA	AAG	CAG	GAA	GAT	GGC	TCC	TTC	GTG	AAA	GTG	GCA	GTG	
Lys	Met	Leu	Lys	Ala	Asp	Ile	Ile	Ala	Ser	Ser	Asp	Ile	1868
AAG	ATG	CTG	AAA	GCT	GAC	ATC	ATT	GCC	TCA	AGC	GAC	ATA	
Glu	Glu	Phe	Leu	Arg	Glu	Ala	Ala	Cys	Met	Lys	Glu	Phe	1907
GAA	GAG	TTC	CTC	CGG	GAA	GCA	GCT	TGC	ATG	AAG	GAG	TTT	
Asp	His	Pro	His	Val	Ala	Lys	Leu	Val	Gly	Val	Ser	Leu	1946
GAC	CAT	CCA	CAC	GTG	GCC	AAG	CTT	GTT	GGG	GTG	AGC	CTC	
Arg	Ser	Arg	Ala	Lys	Gly	Arg	Leu	Pro	Ile	Pro	Met	Val	1985
CGG	AGC	AGG	GCT	AAA	GGT	CGT	CTC	CCC	ATT	CCC	ATG	GTC	
Ile	Leu	Pro	Phe	Met	Lys	His	Gly	Asp	Leu	His	Ala	Phe	2024
ATC	CTG	CCC	TTC	ATG	AAA	CAT	GGA	GAC	TTG	CAC	GCC	TTT	
Leu	Leu	Ala	Ser	Arg	Ile	Gly	Glu	Asn	Pro	Phe	Asn	Leu	2063
CTG	CTC	GCC	TCC	CGA	ATC	GGG	GAG	AAC	CCT	TTT	AAC	CTG	

Pro CCC	Leu CTG	Gln CAG	Thr ACC	Leu CTG	Val GTC	Arg CGG	Phe TTC	Met ATG	Val GTG	Asp GAC	Ile ATT	Ala GCC	2102
Cys TGT	Gly GGC	Met ATG	Glu GAG	Tyr TAC	Leu CTG	Ser AGC	Ser TCC	Arg CGG	Asn AAC	Phe TTC	Ile ATC	His CAC	2141
Arg CGA	Asp GAC	Leu CTA	Ala GCA	Ala GCT	Arg CGG	Asn AAT	Cys TGC	Met ATG	Leu CTG	Ala GCC	Glu GAG	Asp GAC	2180
Met ATG	Thr ACA	Val GTG	Cys TGT	Val GTG	Ala GCT	Asp GAT	Phe TTT	Gly GGA	Leu CTC	Ser TCT	Arg CGG	Lys AAA	2219
Ile ATC	Tyr TAT	Ser AGC	Gly GGG	Asp GAC	Tyr TAT	Tyr TAT	Arg CGT	Gln CAG	Gly GGC	Cys TGT	Ala GCC	Ser TCC	2258
Lys AAA	Leu TTG	Pro CCC	Val GTC	Lys AAG	Trp TGG	Leu CTG	Ala GCC	Leu CTG	Glu GAG	Ser AGC	Leu TTG	Ala GCT	2297
Asp GAC	Asn AAC	Leu TTG	Tyr TAT	Thr ACT	Val GTA	His CAC	Ser AGT	Asp GAT	Val GTG	Trp TGG	Ala GCC	Phe TTC	2336
Gly GGG	Val GTG	Thr ACC	Met ATG	Trp TGG	Glu GAG	Ile ATC	Met ATG	Thr ACT	Arg CGT	Gly GGG	Gln CAG	Thr ACG	2375
Pro CCA	Tyr TAT	Ala GCT	Gly GGC	Ile ATT	Glu GAA	Asn AAT	Ala GCT	Glu GAG	Ile ATT	Tyr TAC	Asn AAC	Tyr TAC	2414
Leu CTC	Ile ATC	Gly GGC	Gly GGG	Asn AAC	Arg CGC	Leu CTG	Lys AAG	Gln CAG	Pro CCT	Pro CCG	Glu GAG	Cys TGC	2453
Met ATG	Glu GAG	Glu GAA	Val GTG	Tyr TAT	Asp GAT	Leu CTC	Met ATG	Tyr TAC	Gln CAG	Cys TGC	Trp TGG	Ser AGC	2492
Ala GCC	Asp GAC	Pro CCC	Lys AAG	Gln CAG	Arg CGC	Pro CCA	Ser AGC	Phe TTC	Thr ACG	Cys TGT	Leu CTG	Arg CGA	2531
Met ATG	Glu GAA	Leu CTG	Glu GAG	Asn AAC	Ile ATT	Leu CTG	Gly GGC	His CAC	Leu CTG	Ser TCT	Val GTG	Leu CTG	2370
Ser TCC	Thr ACC	Ser AGC	Gln CAG	Asp GAC	Pro CCC	Leu TTG	Tyr TAC	Ile ATC	Asn AAC	Ile ATT	Glu GAG	Arg AGA	2609
Ala GCT	Glu GAG	Gln CAG	Pro CCT	Thr ACT	Glu GAG	Ser AGT	Gly GGC	Ser AGC	Pro CCT	Glu GAG	Leu CTG	His CAC	2648
Cys TGT	Gly GGA	Glu GAG	Arg CGA	Ser TCC	Ser AGC	Ser AGC	Glu GAG	Ala GCA	Gly GGG	Asp GAC	Gly GGC	Ser AGT	2687
Gly GGC	Val GTG	Gly GGG	Ala GCA	Val GTA	Gly GGT	Gly GGC	Ile ATC	Pro CCC	Ser AGT	Asp GAC	Ser TCT	Arg CGG	2726
Tyr TAC	Ile ATC	Phe TTC	Ser AGC	Pro CCC	Gly GGA	Gly GGG	Leu CTA	Ser TCC	Glu GAG	Ser TCA	Pro CCA	Gly GGG	2765
Gln CAG	Leu CTG	Glu GAG	Gln CAG	Gln CAG	Pro CCA	Glu GAA	Ser AGC	Pro CCC	Leu CTC	Asn AAT	Glu GAG	Asn AAC	2804
Gln CAG	Arg AGG	Leu CTG	Leu TTG	Leu TTG	Leu CTG	Gln CAG	Gln CAA	Gly GGG	Leu CTA	Leu CTG	Pro CCT	His CAC	2843
Ser AGT	Ser AGC	Cys TGT											2852

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TAACCCTCAGGCAGAGGAAAGTTGGGGCCCCCTGGCTCTGCTGACCACTGTGCTGCCTGAC
TAGGCCCCAGTCTGATCACAGCCCAGGCAGCAAGGTATGGAGGCTCCTGTGGTAGCCCTCC
CAAGCTGTGCTGGCGCCTGGACGGACCAATGCCCAATCCCAGTTCTTCCTGCAGCCGC
TCTGGCCAGCCTGGCATCAGTTCAGGCCTTGCTTAGAGGAGGTAGCCAGAGCTGGTTG

2912
2972
3032
3092

CCTGAATGCAGGCAGCTGGCAGGAGGGGAGGGTGGCTATGTTTCCATGGGTACCATGGGT	3152
GTGGATGGCAGTAAGGGAGGGTAGCAACAGCCCTGTGGGCCCCCTACCCCTCTGGCTGAGC	3212
TGCTCCTACTTTAGTGCATGCTTGGAGCCGCCTGCAGCCTGGAAGCTCAGCACTGCCACC	3272
ACACTTGGGCCGAAATGCCAGGTTTGGCCCTCTTAAGTCACAAAGAGATGTCCATGTATT	3332
GTTCCCTTTTAGGTGATGATTAGGAAGGGATTGGCACACTTGGGTCCCTAAGCCCTATGG	3392
CAGGAAATGGTGGGATATTCTCAGGTCTGAATCCTCATCATCTTCTGATTCCCCACCCT	3452
GCAAAGGCCTGGAAGCTGGCTGTGGGGCTCTGAGGCATGCTGAAGGACAAAAGATTACAGA	3512
GATCCGACTTCAAAAAGGCAGGGTCTGAGTCTGGCAGGTGGAGAGGTGCTAAGGGGCTGGC	3572
CCAGGAGTCAGGCATTTTCAGGACCCCTCCAAGCTTCTACAGTCTGTCTGAGCATGCTACC	3632
AAGCCCCCAGATACCCCCAAAATAACAGAGGCAGTTTTGTCTGAGCCCAGCCCTCCCACA	3692
TGATGACCCCTTAGGTCTACCCTCCTCTCTAAATGGACATCCTCGTTTGTTCCCAAGTCTCC	3752
AGAGAGACTACTGATGGCTGATGTGGGTAAGAAAAGTTCCAGGAACCAGGGCTGGGGTGG	3812
AACGAGGGCTGGGGTCGAGGCAGGCTCTTGGGCAGGCTCTTGCTGTAGGAACATTTCTA	3872
AGCTATTAAGTTGCTGTTTCAAAACAAATAAAATTGAAACATAAAGA _n	3919

(9) INFORMATION FOR SEQUENCE ID NO. 8:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2550 BASE PAIRS

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: cDNA

(3) SEQUENCE DESCRIPTION: SEQ ID NO. 8:

												Ala	Gly	
												GCA	GGC	6
Leu	Lys	Leu	Met	Gly	Ala	Pro	Val	Lys	Met	Thr	Val	Ser		
CTG	AAG	CTC	ATG	GGC	GCC	CCA	GTG	AAG	ATG	ACC	GTG	TCT		45
Gln	Gly	Gln	Pro	Val	Lys	Leu	Asn	Cys	Ser	Val	Glu	Gly		
CAG	GGG	CAG	CCA	GTG	AAG	CTC	AAC	TGC	AGC	GTG	GAG	GGG		84
Met	Glu	Asp	Pro	Asp	Ile	His	Trp	Met	Lys	Asp	Gly	Thr		
ATG	GAG	GAC	CCT	GAC	ATC	CAC	TGG	ATG	AAG	GAT	GGC	ACC		123
Val	Val	Gln	Asn	Ala	Ser	Gln	Val	Ser	Ile	Ser	Ile	Ser		
GTG	GTC	CAG	AAT	GCA	AGC	CAG	GTG	TCC	ATC	TCC	ATC	AGC		162
Glu	His	Ser	Trp	Ile	Gly	Leu	Leu	Ser	Leu	Lys	Ser	Val		
GAG	CAC	AGC	TGG	ATT	GGC	TTA	CTC	AGC	CTA	AAG	TCA	GTG		201
Glu	Arg	Ser	Asp	Ala	Gly	Leu	Tyr	Trp	Cys	Gln	Val	Lys		
GAG	CGG	TCT	GAT	GCT	GGC	CTG	TAC	TGG	TGC	CAG	GTG	AAG		240
Asp	Gly	Glu	Glu	Thr	Lys	Ile	Ser	Gln	Ser	Val	Trp	Leu		
GAT	GGG	GAG	GAA	ACC	AAG	ATC	TCT	CAG	TCA	GTA	TGG	CTC		279
Thr	Val	Glu	Gly	Val	Pro	Phe	Phe	Thr	Val	Glu	Pro	Lys		
ACT	GTC	GAA	GGT	GTG	CCA	TTC	TTC	ACA	GTG	GAA	CCA	AAA		318
Asp	Leu	Ala	Val	Pro	Pro	Asn	Ala	Pro	Phe	Gln	Leu	Ser		
GAT	CTG	GCG	GTG	CCA	CCC	AAT	GCC	CCT	TTT	CAG	CTG	TCT		357
Cys	Glu	Ala	Val	Gly	Pro	Pro	Glu	Pro	Val	Thr	Ile	Tyr		
TGT	GAG	GCT	GTG	GGT	CCT	CCA	GAA	CCC	GTA	ACC	ATT	TAC		396
Trp	Trp	Arg	Gly	Leu	Thr	Lys	Val	Gly	Gly	Pro	Ala	Pro		
TGG	TGG	AGA	GGA	CTC	ACT	AAA	GTT	GGG	GGA	CCT	GCT	CCC		435

Ser TCT	Pro CCC	Ser TCT	Val GTT	Leu TTA	Asn AAT	Val GTG	Thr ACA	Gly GGA	Val GTG	Thr ACC	Gln CAG	Arg CGC	474
Thr ACA	Glu GAG	Phe TTT	Ser TCT	Cys TGT	Glu GAA	Ala GCC	Arg CGC	Asn AAC	Ile ATA	Lys AAA	Gly GGC	Leu CTG	513
Ala GCC	Thr ACT	Ser TCC	Arg CGA	Pro CCA	Ala GCC	Ile ATT	Val GTT	Arg CGC	Leu CTT	Gln CAA	Ala GCA	Pro CCG	552
Pro CCT	Ala GCA	Ala GCT	Pro CCT	Phe TTC	Asn AAC	Thr ACC	Thr ACA	Val GTA	Thr ACA	Thr ACG	Ile ATC	Ser TCC	591
Ser AGC	Tyr TAC	Asn AAC	Ala GCT	Ser AGC	Val GTG	Ala GCC	Trp TGG	Val GTG	Pro CCA	Gly GGT	Ala GCT	Asp GAC	630
Gly GGC	Leu CTA	Ala GCT	Leu CTG	Leu CTG	His CAT	Ser TCC	Cys TGT	Thr ACT	Val GTA	Gln CAG	Val GTG	Ala GCA	669
His CAC	Ala GCC	Pro CCA	Gly GGA	Glu GAA	Trp TGG	Glu GAG	Ala GCC	Leu CTT	Ala GCT	Val GTT	Val GTG	Val GTT	708
Pro CCT	Val GTG	Pro CCA	Pro CCT	Phe TTT	Thr ACC	Cys TGC	Leu CTG	Leu CTT	Arg CGG	Asn AAC	Leu TTG	Ala GCC	747
Pro CCT	Ala GCC	Thr ACC	Asn AAC	Tyr TAC	Ser AGC	Leu CTT	Arg AGG	Val GTG	Arg CGC	Cys TGT	Ala GCC	Asn AAT	786
Ala GCC	Leu TTG	Gly GGC	Pro CCT	Ser TCT	Pro CCC	Tyr TAC	Gly GGC	Asp GAC	Trp TGG	Val GTG	Pro CCC	Phe TTT	825
Gln CAG	Thr ACA	Lys AAG	Gly GGC	Leu CTA	Ala GCG	Pro CCA	Ala GCC	Arg AGA	Ala GCT	Pro CCT	Gln CAG	Asn AAT	864
Phe TTC	His CAT	Ala GCC	Ile ATT	Arg CGT	Thr ACC	Asp GAC	Ser TCA	Gly GGC	Leu CTT	Ile ATC	Leu CTG	Glu GAA	903
Trp TGG	Glu GAA	Glu GAA	Val GTG	Ile ATT	Pro CCT	Glu GAG	Asp GAC	Pro CCT	Gly GGG	Glu GAA	Gly GGC	Pro CCC	942
Leu CTA	Gly GGA	Pro CCT	Tyr TAT	Lys AAG	Leu CTG	Ser TCC	Trp TGG	Val GTC	Gln CAA	Glu GAA	Asn AAT	Gly GGA	981
Thr ACC	Gln CAG	Asp GAT	Glu GAG	Leu CTG	Met ATG	Val GTG	Glu GAA	Gly GGG	Thr ACC	Arg AGG	Ala GCC	Asn AAT	1020
Leu CTG	Thr ACC	Asp GAC	Trp TGG	Asp GAT	Pro CCC	Gln CAG	Lys AAG	Asp GAC	Leu CTG	Ile ATT	Leu TTG	Arg CGT	1059
Val GTG	Cys TGT	Ala GCC	Ser TCC	Asn AAT	Ala GCA	Ile ATT	Gly GGT	Asp GAT	Gly GGG	Pro CCC	Trp TGG	Ser AGT	1098
Gln CAG	Pro CCA	Leu CTG	Val GTG	Val GTG	Ser TCT	Ser TCT	His CAT	Asp GAC	His CAT	Ala GCA	Gly GGG	Arg AGG	1137
Gln CAG	Gly GGC	Pro CCT	Pro CCC	His CAC	Ser AGC	Arg CGC	Thr ACA	Ser TCC	Trp TGG	Val GTG	Pro CCT	Val GTG	1176
Val GTC	Leu CTG	Gly GGC	Val GTG	Leu CTC	Thr ACC	Ala GCC	Leu CTG	Ile ATC	Thr ACA	Ala GCT	Ala GCT	Ala GCC	1215
Leu TTG	Ala GCC	Leu CTC	Ile ATC	Leu CTG	Leu CTT	Arg CGG	Lys AAG	Arg AGA	Arg CGC	Lys AAG	Glu GAG	Thr ACG	1254
Arg CGT	Phe TTC	Gly GGG	Gln CAA	Ala GCC	Phe TTT	Asp GAC	Ser AGT	Val GTC	Met ATG	Ala GCC	Arg CGA	Gly GGG	1293
Glu GAG	Pro CCA	Ala GCT	Val GTA	His CAC	Phe TTC	Arg CGG	Ala GCA	Ala GCC	Arg CGA	Ser TCT	Phe TTC	Asn AAT	1332

Arg CGA	Glu GAA	Arg AGG	Pro CCT	Glu GAA	Arg CGC	Ile ATT	Glu GAG	Ala GCC	Thr ACA	Leu TTG	Asp GAT	Ser AGC	1371
Leu CTG	Gly GGC	Ile ATC	Ser AGC	Asp GAT	Glu GAA	Leu TTG	Lys AAG	Glu GAA	Lys AAG	Leu CTG	Glu GAG	Asp GAT	1410
Val GTC	Leu CTC	Ile ATT	Pro CCA	Glu GAG	Gln CAG	Gln CAG	Phe TTC	Thr ACC	Leu CTC	Gly GGT	Arg CGG	Met ATG	1449
Leu TTG	Gly GGC	Lys AAA	Gly GGA	Glu GAG	Phe TTT	Gly GGA	Ser TCA	Val GTG	Arg CGG	Glu GAA	Ala GCC	Gln CAG	1488
Leu CTA	Lys AAG	Gln CAG	Glu GAA	Asp GAT	Gly GGC	Ser TCC	Phe TTC	Val GTG	Lys AAA	Val GTG	Ala GCA	Val GTG	1527
Lys AAG	Met ATG	Leu CTG	Lys AAA	Ala GCT	Asp GAC	Ile ATC	Ile ATT	Ala GCC	Ser TCA	Ser AGC	Asp GAC	Ile ATA	1566
Glu GAA	Glu GAG	Phe TTC	Leu CTC	Arg CGG	Glu GAA	Ala GCA	Ala GCT	Cys TGC	Met ATG	Lys AAG	Glu GAG	Phe TTT	1605
Asp GAC	His CAT	Pro CCA	His CAC	Val GTG	Ala GCC	Lys AAG	Leu CTT	Val GTT	Gly GGG	Val GTG	Ser AGC	Leu CTC	1644
Arg CGG	Ser AGC	Arg AGG	Ala GCT	Lys AAA	Gly GGT	Arg CGT	Leu CTC	Pro CCC	Ile ATT	Pro CCC	Met ATG	Val GTC	1683
Ile ATC	Leu CTG	Pro CCC	Phe TTC	Met ATG	Lys AAA	His CAT	Gly GGA	Asp GAC	Leu TTG	His CAC	Ala GCC	Phe TTT	1722
Leu CTG	Leu CTC	Ala GCC	Ser TCC	Arg CGA	Ile ATC	Gly GGG	Glu GAG	Asn AAC	Pro CCT	Phe TTT	Asn AAC	Leu CTG	1761
Pro CCC	Leu CTG	Gln CAG	Thr ACC	Leu CTG	Val GTC	Arg CGG	Phe TTC	Met ATG	Val GTG	Asp GAC	Ile ATT	Ala GCC	1800
Cys TGT	Gly GGC	Met ATG	Glu GAG	Tyr TAC	Leu CTG	Ser AGC	Ser TCC	Arg CGG	Asn AAC	Phe TTC	Ile ATC	His CAC	1839
Arg CGA	Asp GAC	Leu CTA	Ala GCA	Ala GCT	Arg CGG	Asn AAT	Cys TGC	Met ATG	Leu CTG	Ala GCC	Glu GAG	Asp GAC	1878
Met ATG	Thr ACA	Val GTG	Cys TGT	Val GTG	Ala GCT	Asp GAT	Phe TTT	Gly GGA	Leu CTC	Ser TCT	Arg CGG	Lys AAA	1917
Ile ATC	Tyr TAT	Ser AGC	Gly GGG	Asp GAC	Tyr TAT	Tyr TAT	Arg CGT	Gln CAG	Gly GGC	Cys TGT	Ala GCC	Ser TCC	1956
Lys AAA	Leu TTG	Pro CCC	Val GTC	Lys AAG	Trp TGG	Leu CTG	Ala GCC	Leu CTG	Glu GAG	Ser AGC	Leu TTG	Ala GCT	1995
Asp GAC	Asn AAC	Leu TTG	Tyr TAT	Thr ACT	Val GTA	His CAC	Ser AGT	Asp GAT	Val GTG	Trp TGG	Ala GCC	Phe TTC	2034
Gly GGG	Val GTG	Thr ACC	Met ATG	Trp TGG	Glu GAG	Ile ATC	Met ATG	Thr ACT	Arg CGT	Gly GGG	Gln CAG	Thr ACG	2073
Pro CCA	Tyr TAT	Ala GCT	Gly GGC	Ile ATT	Glu GAA	Asn AAT	Ala GCT	Glu GAG	Ile ATT	Tyr TAC	Asn AAC	Tyr TAC	2112
Leu CTC	Ile ATC	Gly GGC	Gly GGG	Asn AAC	Arg CGC	Leu CTG	Lys AAG	Gln CAG	Pro CCT	Pro CCG	Glu GAG	Cys TGC	2151
Met ATG	Glu GAG	Glu GAA	Val GTG	Tyr TAT	Asp GAT	Leu CTC	Met ATG	Tyr TAC	Gln CAG	Cys TGC	Trp TGG	Ser AGC	2190
Ala GCC	Asp GAC	Pro CCC	Lys AAG	Gln CAG	Arg CGC	Pro CCA	Ser AGC	Phe TTC	Thr ACG	Cys TGT	Leu CTG	Arg CGA	2229

Met	Glu	Leu	Glu	Asn	Ile	Leu	Gly	His	Leu	Ser	Val	Leu	
ATG	GAA	CTG	GAG	AAC	ATT	CTG	GGC	CAC	CTG	TCT	GTG	CTG	2268
Ser	Thr	Ser	Gln	Asp	Pro	Leu	Tyr	Ile	Asn	Ile	Glu	Arg	
TCC	ACC	AGC	CAG	GAC	CCC	TTG	TAC	ATC	AAC	ATT	GAG	AGA	2307
Ala	Glu	Gln	Pro	Thr	Glu	Ser	Gly	Ser	Pro	Glu	Leu	His	
GCT	GAG	CAG	CCT	ACT	GAG	AGT	GGC	AGC	CCT	GAG	CTG	CAC	2346
Cys	Gly	Glu	Arg	Ser	Ser	Ser	Glu	Ala	Gly	Asp	Gly	Ser	
TGT	GGA	GAG	CGA	TCC	AGC	AGC	GAG	GCA	GGG	GAC	GGC	AGT	2385
Gly	Val	Gly	Ala	Val	Gly	Gly	Ile	Pro	Ser	Asp	Ser	Arg	
GGC	GTG	GGG	GCA	GTA	GGT	GGC	ATC	CCC	AGT	GAC	TCT	CGG	2424
Tyr	Ile	Phe	Ser	Pro	Gly	Gly	Leu	Ser	Glu	Ser	Pro	Gly	
TAC	ATC	TTC	AGC	CCC	GGA	GGG	CTA	TCC	GAG	TCA	CCA	GGG	2463
Gln	Leu	Glu	Gln	Gln	Pro	Glu	Ser	Pro	Leu	Asn	Glu	Asn	
CAG	CTG	GAG	CAG	CAG	CCA	GAA	AGC	CCC	CTC	AAT	GAG	AAC	2502
Gln	Arg	Leu	Leu	Leu	Leu	Gln	Gln	Gly	Leu	Leu	Pro	His	
CAG	AGG	CTG	TTG	TTG	CTG	CAG	CAA	GGG	CTA	CTG	CCT	CAC	2541
Ser	Ser	Cys											
AGT	AGC	TGT											2550

(10) INFORMATION FOR SEQUENCE ID NO. 9:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4364 BASE PAIRS

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: cDNA

(3) SEQUENCE DESCRIPTION: SEQ ID NO. 9:

CATTAGATCTTTACATGAAAGTAAAATTTATAAGATTTCTAGAAAGTCAAAAGATGATAA	60
CTATTTCTTAGGATACTAAAAGCACTCACATTATAGAAAAAATCAGTTAACTATACTC	120
CACAAACATTAAAGGCTCCCTATAAAAAAACATTTTTAATAGGCAAGCCACAGAAAGGGC	180
AAATATTAATAGTTTGCAATACATATGTATGAAAAGGAATTGAATCTAGAATATTTAACA	240
AAGCTTTACAACCTCAAAAAATACAAAGAAAAATATTTTCTTCCAATTGGCAAATTACTTA	300
AACAGAACCTTCACAAAAGAAGATAAGAATGTTTAAATAACATTTGAAGCCATAATAATG	360
ACATCATTAGCCATGATGGAAATGCAAATTTAAGTACCACTTCACATCCACAAGAAAAAG	420
ATAAAAAATAAAAGGACTGAGCTCACCAAAACATTGGTGAGGATGTGGTAATACTGAAATTC	480
TTGTACCGTGCTCCTGAGGGTATAACATATTACAGGATTTTTTTGAAACTAGTGGTTCC	540
TTATAAACTTAATGCCCTGGCAACCTCACACCTATTACTTAAGAATGAAAGGGCCCCGC	600
CCTCCTCCCTCCTCGCTCGCGGGCCGGGCCGCGATGGTGCGGCGTCGCCCGCATGGCG	660
CTGAGGCGGAGC	672
Met Gly Arg Pro Gly Leu Pro Pro Leu Pro Leu Pro Pro	
ATG GGG CGG CCG GGG CTC CCG CCG CTG CCG CTG CCG CCG	711
Pro Pro Arg Leu Gly Leu Leu Leu Ala Glu Ser Ala Ala	
CCA CCG CGG CTC GGG CTG CTG CTG GCG GAG TCC GCC GCC	750
Ala Gly Leu Lys Leu Met Gly Ala Pro Val Lys Leu Thr	
GCA GGT CTG AAG CTC ATG GGA GCC CCG GTG AAG CTG ACA	789
Val Ser Gln Gly Gln Pro Val Lys Leu Asn Cys Ser Val	
GTG TCT CAG GGG CAG CCG GTG AAG CTC AAC TGC AGT GTG	828

Glu	Gly	Met	Glu	Glu	Pro	Asp	Ile	Gln	Trp	Val	Lys	Asp	867
GAG	GGG	ATG	GAG	GAG	CCT	GAC	ATC	CAG	TGG	GTG	AAG	GAT	
Gly	Ala	Val	Val	Gln	Asn	Leu	Asp	Gln	Leu	Tyr	Ile	Pro	906
GGG	GCT	GTG	GTC	CAG	AAC	TTG	GAC	CAG	TTG	TAC	ATC	CCA	
Val	Ser	Glu	Gln	His	Trp	Ile	Gly	Phe	Leu	Ser	Leu	Lys	945
GTC	AGC	GAG	CAG	CAC	TGG	ATC	GGC	TTC	CTC	AGC	CTG	AAG	
Ser	Val	Glu	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Trp	Cys	Gln	984
TCA	GTG	GAG	CGC	TCT	GAC	GCC	GGC	CGG	TAC	TGG	TGC	CAG	
Val	Glu	Asp	Gly	Gly	Glu	Thr	Glu	Ile	Ser	Gln	Pro	Val	1023
GTG	GAG	GAT	GGG	GGT	GAA	ACC	GAG	ATC	TCC	CAG	CCA	GTG	
Trp	Leu	Thr	Val	Glu	Gly	Val	Pro	Phe	Phe	Thr	Val	Glu	1062
TGG	CTC	ACG	GTA	GAA	GGT	GTG	CCA	TTT	TTC	ACA	GTG	GAG	
Pro	Lys	Asp	Leu	Ala	Val	Pro	Pro	Asn	Ala	Pro	Phe	Gln	1101
CCA	AAA	GAT	CTG	GCA	GTG	CCA	CCC	AAT	GCC	CCT	TTC	CAA	
Leu	Ser	Cys	Glu	Ala	Val	Gly	Pro	Pro	Glu	Pro	Val	Thr	1140
CTG	TCT	TGT	GAG	GCT	GTG	GGT	CCC	CCT	GAA	CCT	GTT	ACC	
Ile	Val	Trp	Trp	Arg	Gly	Thr	Thr	Lys	Ile	Gly	Gly	Pro	1179
ATT	GTC	TGG	TGG	AGA	GGA	ACT	ACG	AAG	ATC	GGG	GGA	CCC	
Ala	Pro	Ser	Pro	Ser	Val	Leu	Asn	Val	Thr	Gly	Val	Thr	1218
GCT	CCC	TCT	CCA	TCT	GTT	TTA	AAT	GTA	ACA	GGG	GTG	ACC	
Gln	Ser	Thr	Met	Phe	Ser	Cys	Glu	Ala	His	Asn	Leu	Lys	1257
CAG	AGC	ACC	ATG	TTT	TCC	TGT	GAA	GCT	CAC	AAC	CTA	AAA	
Gly	Leu	Ala	Ser	Ser	Arg	Thr	Ala	Thr	Val	His	Leu	Gln	1296
GGC	CTG	GCC	TCT	TCT	CGC	ACA	GCC	ACT	GTT	CAC	CTT	CAA	
Ala	Leu	Pro	Ala	Ala	Pro	Phe	Asn	Ile	Thr	Val	Thr	Lys	1335
GCA	CTG	CCT	GCA	GCC	CCC	TTC	AAC	ATC	ACC	GTG	ACA	AAG	
Leu	Ser	Ser	Ser	Asn	Ala	Ser	Val	Ala	Trp	Met	Pro	Gly	1374
CTT	TCC	AGC	AGC	AAC	GCT	AGT	GTG	GCC	TGG	ATG	CCA	GGT	
Ala	Asp	Gly	Arg	Ala	Leu	Leu	Gln	Ser	Cys	Thr	Val	Gln	1413
GCT	GAT	GGC	CGA	GCT	CTG	CTA	CAG	TCC	TGT	ACA	GTT	CAG	
Val	Thr	Gln	Ala	Pro	Gly	Gly	Trp	Glu	Val	Leu	Ala	Val	1452
GTG	ACA	CAG	GCC	CCA	GGA	GGC	TGG	GAA	GTC	CTG	GCT	GTT	
Val	Val	Pro	Val	Pro	Pro	Phe	Thr	Cys	Leu	Leu	Arg	Asp	1491
GTG	GTC	CCT	GTG	CCC	CCC	TTT	ACC	TGC	CTG	CTC	CGG	GAC	
Leu	Val	Pro	Ala	Thr	Asn	Tyr	Ser	Leu	Arg	Val	Arg	Cys	1530
CTG	GTG	CCT	GCC	ACC	AAC	TAC	AGC	CTC	AGG	GTG	CGC	TGT	
Ala	Asn	Ala	Leu	Gly	Pro	Ser	Pro	Tyr	Ala	Asp	Trp	Val	1569
GCC	AAT	GCC	TTG	GGG	CCC	TCT	CCC	TAT	GCT	GAC	TGG	GTG	
Pro	Phe	Gln	Thr	Lys	Gly	Leu	Ala	Pro	Ala	Ser	Ala	Pro	1608
CCC	TTT	CAG	ACC	AAG	GGT	CTA	GCC	CCA	GCC	AGC	GCT	CCC	
Gln	Asn	Leu	His	Ala	Ile	Arg	Thr	Asp	Ser	Gly	Leu	Ile	1647
CAA	AAC	CTC	CAT	GCC	ATC	CGC	ACA	GAT	TCA	GGC	CTC	ATC	
Leu	Glu	Trp	Glu	Glu	Val	Ile	Pro	Glu	Ala	Pro	Leu	Glu	1686
TTG	GAG	TGG	GAA	GAA	GTG	ATC	CCC	GAG	GCC	CCT	TTG	GAA	
Gly	Pro	Leu	Gly	Pro	Tyr	Lys	Leu	Ser	Trp	Val	Gln	Asp	1725
GGC	CCC	CTG	GGA	CCC	TAC	AAA	CTG	TCC	TGG	GTT	CAA	GAC	

Asn AAT	Gly GGA	Thr ACC	Gln CAG	Asp GAT	Glu GAG	Leu CTG	Thr ACA	Val GTG	Glu GAG	Gly GGG	Thr ACC	Arg AGG	1764
Ala GCC	Asn AAT	Leu TTG	Thr ACA	Gly GGC	Trp TGG	Asp GAT	Pro CCC	Gln CAA	Lys AAG	Asp GAC	Leu CTG	Ile ATC	1803
Val GTA	Arg CGT	Val GTG	Cys TGC	Val GTC	Ser TCC	Asn AAT	Ala GCA	Val GTT	Gly GGC	Cys TGT	Gly GGA	Pro CCC	1842
Trp TGG	Ser AGT	Gln CAG	Pro CCA	Leu CTG	Val GTG	Val GTC	Ser TCT	Ser TCT	His CAT	Asp GAC	Arg CGT	Ala GCA	1881
Gly GGC	Gln CAG	Gln CAG	Gly GGC	Pro CCT	Pro CCT	His CAC	Ser AGC	Arg CGC	Thr ACA	Ser TCC	Trp TGG	Val GTA	1920
Pro CCT	Val GTG	Val GTC	Leu CTT	Gly GGT	Val GTG	Leu CTA	Thr ACG	Ala GCC	Leu CTG	Val GTG	Thr ACG	Ala GCT	1959
Ala GCT	Ala GCC	Leu CTG	Ala GCC	Leu CTC	Ile ATC	Leu CTG	Leu CTT	Arg CGA	Lys AAG	Arg AGA	Arg CGG	Lys AAA	1998
Glu GAG	Thr ACG	Arg CGG	Phe TTT	Gly GGG	Gln CAA	Ala GCC	Phe TTT	Asp GAC	Ser AGT	Val GTC	Met ATG	Ala GCC	2037
Arg CGG	Gly GGA	Glu GAG	Pro CCA	Ala GCC	Val GTT	His CAC	Phe TTC	Arg CGG	Ala GCA	Ala GCC	Arg CGG	Ser TCC	2076
Phe TTC	Asn AAT	Arg CGA	Glu GAA	Arg AGG	Pro CCC	Glu GAG	Arg CGC	Ile ATC	Glu GAG	Ala GCC	Thr ACA	Leu TTG	2115
Asp GAC	Ser AGC	Leu TTG	Gly GGC	Ile ATC	Ser AGC	Asp GAT	Glu GAA	Leu CTA	Lys AAG	Glu GAA	Lys AAA	Leu CTG	2154
Glu GAG	Asp GAT	Val GTG	Leu CTC	Ile ATC	Pro CCA	Glu GAG	Gln CAG	Gln CAG	Phe TTC	Thr ACC	Leu CTG	Gly GGC	2193
Arg CGG	Met ATG	Leu TTG	Gly GGC	Lys AAA	Gly GGA	Glu GAG	Phe TTT	Gly GGT	Ser TCA	Val GTG	Arg CGG	Glu GAG	2232
Ala GCC	Gln CAG	Leu CTG	Lys AAG	Gln CAA	Glu GAG	Asp GAT	Gly GGC	Ser TCC	Phe TTT	Val GTG	Lys AAA	Val GTG	2271
Ala GCT	Val GTG	Lys AAG	Met ATG	Leu CTG	Lys AAA	Ala GCT	Asp GAC	Ile ATC	Ile ATT	Ala GCC	Ser TCA	Ser AGC	2310
Asp GAC	Ile ATT	Glu GAA	Glu GAG	Phe TTC	Leu CTC	Arg AGG	Glu GAA	Ala GCA	Ala GCT	Cys TGC	Met ATG	Lys AAG	2349
Glu GAG	Phe TTT	Asp GAC	His CAT	Pro CCA	His CAC	Val GTG	Ala GCC	Lys AAA	Leu CTT	Val GTT	Gly GGG	Val GTA	2388
Ser AGC	Leu CTC	Arg CGG	Ser AGC	Arg AGG	Ala GCT	Lys AAA	Gly GGC	Arg CGT	Leu CTC	Pro CCC	Ile ATC	Pro CCC	2427
Met ATG	Val GTC	Ile ATC	Leu TTG	Pro CCC	Phe TTC	Met ATG	Lys AAG	His CAT	Gly GGG	Asp GAC	Leu CTG	His CAT	2466
Ala GCC	Phe TTC	Leu CTG	Leu CTC	Ala GCC	Ser TCC	Arg CGG	Ile ATT	Gly GGG	Glu GAG	Asn AAC	Pro CCC	Phe TTT	2505
Asn AAC	Leu CTA	Pro CCC	Leu CTC	Gln CAG	Thr ACC	Leu CTG	Ile ATC	Arg CGG	Phe TTC	Met ATG	Val GTG	Asp GAC	2544
Ile ATT	Ala GCC	Cys TGC	Gly GGC	Met ATG	Glu GAG	Tyr TAC	Leu CTG	Ser AGC	Ser TCT	Arg CGG	Asn AAC	Phe TTC	2583
Ile ATC	His CAC	Arg CGA	Asp GAC	Leu CTG	Ala GCT	Ala GCT	Arg CGG	Asn AAT	Cys TGC	Met ATG	Leu CTG	Ala GCA	2622

Glu	Asp	Met	Thr	Val	Cys	Val	Ala	Asp	Phe	Gly	Leu	Ser	
GAG	GAC	ATG	ACA	GTG	TGT	GTG	GCT	GAC	TTC	GGA	CTC	TCC	2661
Arg	Lys	Ile	Tyr	Ser	Gly	Asp	Tyr	Tyr	Arg	Gln	Gly	Cys	
CGG	AAG	ATC	TAC	AGT	GGG	GAC	TAC	TAT	CGT	CAA	GGC	TGT	2700
Ala	Ser	Lys	Leu	Pro	Val	Lys	Trp	Leu	Ala	Leu	Glu	Ser	
GCC	TCC	AAA	CTG	CCT	GTC	AAG	TGG	CTG	GCC	CTG	GAG	AGC	2739
Leu	Ala	Asp	Asn	Leu	Tyr	Thr	Val	Gln	Ser	Asp	Val	Trp	
CTG	GCC	GAC	AAC	CTG	TAT	ACT	GTG	CAG	AGT	GAC	GTG	TGG	2778
Ala	Phe	Gly	Val	Thr	Met	Trp	Glu	Ile	Met	Thr	Arg	Gly	
GCG	TTC	GGG	GTG	ACC	ATG	TGG	GAG	ATC	ATG	ACA	CGT	GGG	2817
Gln	Thr	Pro	Tyr	Ala	Gly	Ile	Glu	Asn	Ala	Glu	Ile	Tyr	
CAG	ACG	CCA	TAT	GCT	GGC	ATC	GAA	AAC	GCT	GAG	ATT	TAC	2856
Asn	Tyr	Leu	Ile	Gly	Gly	Asn	Arg	Leu	Lys	Gln	Pro	Pro	
AAC	TAC	CTC	ATT	GGC	GGG	AAC	CGC	CTG	AAA	CAG	CCT	CCG	2895
Glu	Cys	Met	Glu	Asp	Val	Tyr	Asp	Leu	Met	Tyr	Gln	Cys	
GAG	TGT	ATG	GAG	GAC	GTG	TAT	GAT	CTC	ATG	TAC	CAG	TGC	2934
Trp	Ser	Ala	Asp	Pro	Lys	Gln	Arg	Pro	Ser	Phe	Thr	Cys	
TGG	AGT	GCT	GAC	CCC	AAG	CAG	CGC	CCG	AGC	TTT	ACT	TGT	2973
Leu	Arg	Met	Glu	Leu	Glu	Asn	Ile	Leu	Gly	Gln	Leu	Ser	
CTG	CGA	ATG	GAA	CTG	GAG	AAC	ATC	TTG	GGC	CAG	CTG	TCT	3012
Val	Leu	Ser	Ala	Ser	Gln	Asp	Pro	Leu	Tyr	Ile	Asn	Ile	
GTG	CTA	TCT	GCC	AGC	CAG	GAC	CCC	TTA	TAC	ATC	AAC	ATC	3051
Glu	Arg	Ala	Glu	Glu	Pro	Thr	Val	Gly	Gly	Ser	Leu	Glu	
GAG	AGA	GCT	GAG	GAG	CCC	ACT	GTG	GGA	GGC	AGC	CTG	GAG	3090
Leu	Pro	Gly	Arg	Asp	Gln	Pro	Tyr	Ser	Gly	Ala	Gly	Asp	
CTA	CCT	GGC	AGG	GAT	CAG	CCC	TAC	AGT	GGG	GCT	GGG	GAT	3129
Gly	Ser	Gly	Met	Gly	Ala	Val	Gly	Gly	Thr	Pro	Ser	Asp	
GGC	AGT	GGC	ATG	GGG	GCA	GTG	GGT	GGC	ACT	CCC	AGT	GAC	3168
Cys	Arg	Tyr	Ile	Leu	Thr	Pro	Gly	Gly	Leu	Ala	Glu	Gln	
TGT	CGG	TAC	ATA	CTC	ACC	CCC	GGA	GGG	CTG	GCT	GAG	CAG	3207
Pro	Gly	Gln	Ala	Glu	His	Gln	Pro	Glu	Ser	Pro	Leu	Asn	
CCA	GGG	CAG	GCA	GAG	CAC	CAG	CCA	GAG	AGT	CCC	CTC	AAT	3246
Glu	Thr	Gln	Arg	Leu	Leu	Leu	Leu	Gln	Gln	Gly	Leu	Leu	
GAG	ACA	CAG	AGG	CTT	TTG	CTG	CTG	CAG	CAA	GGG	CTA	CTG	3285
Pro	His	Ser	Ser	Cys									
CCA	CAC	AGT	AGC	TGT									3300

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TAGCCACAGGCAGAGGGCATCGGGGCCATTTGGCCGGCTCTGGTGGCCACTGAGCTGGC	3360
TGACTAAGCCCCGTCTGACCCAGCCAGACAGCAAGGTGTGGAGGCTCCTGTGGTAGTC	3420
ATCCCAAGCTGTGTGGGAAGCCCGGACTGACCAATACCCAATCCCAGTTCTTCCTGC	3480
CACCACTCTGTGGCCAGCCTGGCATCAGTTTAGGCCTTGGCTTGATGGAAGTGGGCCAGT	3540
CCTGGTTGTCTGAACCCAGGCAGCTGGCAGGAGTGGGGTGGTTATGTTTCCATGGTTACC	3600
ATGGGTGTGGATGGCAGTGTGGGGAGGGCAGGTCCAGCTCTGTGGGCCCTACCCCTCCTGC	3660
TGAGCTGCCCCCTGCTGCTTAAGTGCATGCATTGAGCTGCCTCCAGCCTGGTGGCCCAGCT	3720
ATTACCACACTTGGGGTTTAAATATCCAGGTGTGCCCTCCAGTCAGAAAGAGATGTCC	3780
TTGTAATATTCCCTTTTAGGTGAGGGTTGGTAAGGGGTGGTATCTCAGGTCTGAATCTT	3840
CACCATCTTTCTGATTCCGCACCCTGCCTACGCCAGGAGAAAGTTGAGGGGAGCATGCTTC	3900
CCTGCAGCTGACCGGGTCACACAAAGGCATGCTGGAGTACCCAGCCTATCAGGTGCCCT	3960
CTTCCAAAGGCAGCGTGCCGAGCCAGCAAGAGGAAGGGGTGCTGTGAGGCTTGCCAGGA	4020

GCAAGTGAGGCCGGAGAGGAGTTCAGGAACCCCTTCTCCATACCCACAATCTGAGCACGCT	4080
ACCAAATCTCAAAATATCCTAAGACTAACAAAGGCAGCTGTGTCTGAGCCCAACCCCTTCT	4140
AAACGGTGACCTTTAGTGCCAACTTCCCCTCTAACTGGACAGCCTCTTCTGTCCCAAGTC	4200
TCCAGAGAGAAATCAGGCCTGATGAGGGGGAATTCTTGGAACCTGGACCCAGCCTTGGT	4260
GGGGGAGCCTCTGGAATGCATGGGGCGGGTCTAGCTGTTAGGGACATTCCAAGCTGTT	4320
AGTTGCTGTTTTAAATAGAAATAAAATTGAAGACTAAAGACCTA _n	4364

(11) INFORMATION FOR SEQUENCE ID NO. 10:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2550 BASE PAIRS

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: cDNA

(3) SEQUENCE DESCRIPTION: SEQ ID NO. 10:

Ala	Gly	Leu	Lys	Leu	Met	Gly	Ala	Pro	Val	Lys	Leu	Thr		39
GCA	GGT	CTG	AAG	CTC	ATG	GGA	GCC	CCG	GTG	AAG	CTG	ACA		
Val	Ser	Gln	Gly	Gln	Pro	Val	Lys	Leu	Asn	Cys	Ser	Val		78
GTG	TCT	CAG	GGG	CAG	CCG	GTG	AAG	CTC	AAC	TGC	AGT	GTG		
Glu	Gly	Met	Glu	Glu	Pro	Asp	Ile	Gln	Trp	Val	Lys	Asp		117
GAG	GGG	ATG	GAG	GAG	CCT	GAC	ATC	CAG	TGG	GTG	AAG	GAT		
Gly	Ala	Val	Val	Gln	Asn	Leu	Asp	Gln	Leu	Tyr	Ile	Pro		156
GGG	GCT	GTG	GTC	CAG	AAC	TTG	GAC	CAG	TTG	TAC	ATC	CCA		
Val	Ser	Glu	Gln	His	Trp	Ile	Gly	Phe	Leu	Ser	Leu	Lys		195
GTC	AGC	GAG	CAG	CAC	TGG	ATC	GGC	TTC	CTC	AGC	CTG	AAG		
Ser	Val	Glu	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Trp	Cys	Gln		234
TCA	GTG	GAG	CGC	TCT	GAC	GCC	GGC	CGG	TAC	TGG	TGC	CAG		
Val	Glu	Asp	Gly	Gly	Glu	Thr	Glu	Ile	Ser	Gln	Pro	Val		273
GTG	GAG	GAT	GGG	GGT	GAA	ACC	GAG	ATC	TCC	CAG	CCA	GTG		
Trp	Leu	Thr	Val	Glu	Gly	Val	Pro	Phe	Phe	Thr	Val	Glu		312
TGG	CTC	ACG	GTA	GAA	GGT	GTG	CCA	TTT	TTC	ACA	GTG	GAG		
Pro	Lys	Asp	Leu	Ala	Val	Pro	Pro	Asn	Ala	Pro	Phe	Gln		351
CCA	AAA	GAT	CTG	GCA	GTG	CCA	CCC	AAT	GCC	CCT	TTC	CAA		
Leu	Ser	Cys	Glu	Ala	Val	Gly	Pro	Pro	Glu	Pro	Val	Thr		390
CTG	TCT	TGT	GAG	GCT	GTG	GGT	CCC	CCT	GAA	CCT	GTT	ACC		
Ile	Val	Trp	Trp	Arg	Gly	Thr	Thr	Lys	Ile	Gly	Gly	Pro		429
ATT	GTC	TGG	TGG	AGA	GGA	ACT	ACG	AAG	ATC	GGG	GGA	CCC		
Ala	Pro	Ser	Pro	Ser	Val	Leu	Asn	Val	Thr	Gly	Val	Thr		468
GCT	CCC	TCT	CCA	TCT	GTT	TTA	AAT	GTA	ACA	GGG	GTG	ACC		
Gln	Ser	Thr	Met	Phe	Ser	Cys	Glu	Ala	His	Asn	Leu	Lys		507
CAG	AGC	ACC	ATG	TTT	TCC	TGT	GAA	GCT	CAC	AAC	CTA	AAA		
Gly	Leu	Ala	Ser	Ser	Arg	Thr	Ala	Thr	Val	His	Leu	Gln		546
GGC	CTG	GCC	TCT	TCT	CGC	ACA	GCC	ACT	GTT	CAC	CTT	CAA		

Ala	Leu	Pro	Ala	Ala	Pro	Phe	Asn	Ile	Thr	Val	Thr	Lys	585
GCA	CTG	CCT	GCA	GCC	CCC	TTC	AAC	ATC	ACC	GTG	ACA	AAG	
Leu	Ser	Ser	Ser	Asn	Ala	Ser	Val	Ala	Trp	Met	Pro	Gly	624
CTT	TCC	AGC	AGC	AAC	GCT	AGT	GTG	GCC	TGG	ATG	CCA	GGT	
Ala	Asp	Gly	Arg	Ala	Leu	Leu	Gln	Ser	Cys	Thr	Val	Gln	663
GCT	GAT	GGC	CGA	GCT	CTG	CTA	CAG	TCC	TGT	ACA	GTT	CAG	
Val	Thr	Gln	Ala	Pro	Gly	Gly	Trp	Glu	Val	Leu	Ala	Val	702
GTG	ACA	CAG	GCC	CCA	GGA	GGC	TGG	GAA	GTC	CTG	GCT	GTT	
Val	Val	Pro	Val	Pro	Pro	Phe	Thr	Cys	Leu	Leu	Arg	Asp	741
GTG	GTC	CCT	GTG	CCC	CCC	TTT	ACC	TGC	CTG	CTC	CGG	GAC	
Leu	Val	Pro	Ala	Thr	Asn	Tyr	Ser	Leu	Arg	Val	Arg	Cys	780
CTG	GTG	CCT	GCC	ACC	AAC	TAC	AGC	CTC	AGG	GTG	CGC	TGT	
Ala	Asn	Ala	Leu	Gly	Pro	Ser	Pro	Tyr	Ala	Asp	Trp	Val	819
GCC	AAT	GCC	TTG	GGG	CCC	TCT	CCC	TAT	GCT	GAC	TGG	GTG	
Pro	Phe	Gln	Thr	Lys	Gly	Leu	Ala	Pro	Ala	Ser	Ala	Pro	858
CCC	TTT	CAG	ACC	AAG	GGT	CTA	GCC	CCA	GCC	AGC	GCT	CCC	
Gln	Asn	Leu	His	Ala	Ile	Arg	Thr	Asp	Ser	Gly	Leu	Ile	897
CAA	AAC	CTC	CAT	GCC	ATC	CGC	ACA	GAT	TCA	GGC	CTC	ATC	
Leu	Glu	Trp	Glu	Glu	Val	Ile	Pro	Glu	Ala	Pro	Leu	Glu	936
TTG	GAG	TGG	GAA	GAA	GTG	ATC	CCC	GAG	GCC	CCT	TTG	GAA	
Gly	Pro	Leu	Gly	Pro	Tyr	Lys	Leu	Ser	Trp	Val	Gln	Asp	975
GGC	CCC	CTG	GGA	CCC	TAC	AAA	CTG	TCC	TGG	GTT	CAA	GAC	
Asn	Gly	Thr	Gln	Asp	Glu	Leu	Thr	Val	Glu	Gly	Thr	Arg	1014
AAT	GGA	ACC	CAG	GAT	GAG	CTG	ACA	GTG	GAG	GGG	ACC	AGG	
Ala	Asn	Leu	Thr	Gly	Trp	Asp	Pro	Gln	Lys	Asp	Leu	Ile	1053
GCC	AAT	TTG	ACA	GCC	TGG	GAT	CCC	CAA	AAG	GAC	CTG	ATC	
Val	Arg	Val	Cys	Val	Ser	Asn	Ala	Val	Gly	Cys	Gly	Pro	1092
GTA	CGT	GTG	TGC	GTC	TCC	AAT	GCA	GTT	GGC	TGT	GGA	CCC	
Trp	Ser	Gln	Pro	Leu	Val	Val	Ser	Ser	His	Asp	Arg	Ala	1131
TGG	AGT	CAG	CCA	CTG	GTG	GTC	TCT	TCT	CAT	GAC	CGT	GCA	
Gly	Gln	Gln	Gly	Pro	Pro	His	Ser	Arg	Thr	Ser	Trp	Val	1170
GGC	CAG	CAG	GGC	CCT	CCT	CAC	AGC	CGC	ACA	TCC	TGG	GTA	
Pro	Val	Val	Leu	Gly	Val	Leu	Thr	Ala	Leu	Val	Thr	Ala	1209
CCT	GTG	GTC	CTT	GGT	GTG	CTA	ACG	GCC	CTG	GTG	ACG	GCT	
Ala	Ala	Leu	Ala	Leu	Ile	Leu	Leu	Arg	Lys	Arg	Arg	Lys	1248
GCT	GCC	CTG	GCC	CTC	ATC	CTG	CTT	CGA	AAG	AGA	CGG	AAA	
Glu	Thr	Arg	Phe	Gly	Gln	Ala	Phe	Asp	Ser	Val	Met	Ala	1287
GAG	ACG	CGG	TTT	GGG	CAA	GCC	TTT	GAC	AGT	GTC	ATG	GCC	
Arg	Gly	Glu	Pro	Ala	Val	His	Phe	Arg	Ala	Ala	Arg	Ser	1326
CGG	GGA	GAG	CCA	GCC	GTT	CAC	TTC	CGG	GCA	GCC	CGG	TCC	
Phe	Asn	Arg	Glu	Arg	Pro	Glu	Arg	Ile	Glu	Ala	Thr	Leu	1365
TTC	AAT	CGA	GAA	AGG	CCC	GAG	CGC	ATC	GAG	GCC	ACA	TTG	
Asp	Ser	Leu	Gly	Ile	Ser	Asp	Glu	Leu	Lys	Glu	Lys	Leu	1404
GAC	AGC	TTG	GGC	ATC	AGC	GAT	GAA	CTA	AAG	GAA	AAA	CTG	
Glu	Asp	Val	Leu	Ile	Pro	Glu	Gln	Gln	Phe	Thr	Leu	Gly	1443
GAG	GAT	GTG	CTC	ATC	CCA	GAG	CAG	CAG	TTC	ACC	CTG	GGC	

Arg CGG	Met ATG	Leu TTG	Gly GGC	Lys AAA	Gly GGA	Glu GAG	Phe TTT	Gly GGT	Ser TCA	Val GTG	Arg CGG	Glu GAG	1482
Ala GCC	Gln CAG	Leu CTG	Lys AAG	Gln CAA	Glu GAG	Asp GAT	Gly GGC	Ser TCC	Phe TTT	Val GTG	Lys AAA	Val GTG	1521
Ala GCT	Val GTG	Lys AAG	Met ATG	Leu CTG	Lys AAA	Ala GCT	Asp GAC	Ile ATC	Ile ATT	Ala GCC	Ser TCA	Ser AGC	1560
Asp GAC	Ile ATT	Glu GAA	Glu GAG	Phe TTC	Leu CTC	Arg AGG	Glu GAA	Ala GCA	Ala GCT	Cys TGC	Met ATG	Lys AAG	1599
Glu GAG	Phe TTT	Asp GAC	His CAT	Pro CCA	His CAC	Val GTG	Ala GCC	Lys AAA	Leu CTT	Val GTT	Gly GGG	Val GTA	1638
Ser AGC	Leu CTC	Arg CGG	Ser AGC	Arg AGG	Ala GCT	Lys AAA	Gly GGC	Arg CGT	Leu CTC	Pro CCC	Ile ATC	Pro CCC	1677
Met ATG	Val GTC	Ile ATC	Leu TTG	Pro CCC	Phe TTC	Met ATG	Lys AAG	His CAT	Gly GGG	Asp GAC	Leu CTG	His CAT	1716
Ala GCC	Phe TTC	Leu CTG	Leu CTC	Ala GCC	Ser TCC	Arg CGG	Ile ATT	Gly GGG	Glu GAG	Asn AAC	Pro CCC	Phe TTT	1755
Asn AAC	Leu CTA	Pro CCC	Leu CTC	Gln CAG	Thr ACC	Leu CTG	Ile ATC	Arg CGG	Phe TTC	Met ATG	Val GTG	Asp GAC	1794
Ile ATT	Ala GCC	Cys TGC	Gly GGC	Met ATG	Glu GAG	Tyr TAC	Leu CTG	Ser AGC	Ser TCT	Arg CGG	Asn AAC	Phe TTC	1833
Ile ATC	His CAC	Arg CGA	Asp GAC	Leu CTG	Ala GCT	Ala GCT	Arg CGG	Asn AAT	Cys TGC	Met ATG	Leu CTG	Ala GCA	1872
Glu GAG	Asp GAC	Met ATG	Thr ACA	Val GTG	Cys TGT	Val GTG	Ala GCT	Asp GAC	Phe TTC	Gly GGA	Leu CTC	Ser TCC	1911
Arg CGG	Lys AAG	Ile ATC	Tyr TAC	Ser AGT	Gly GGG	Asp GAC	Tyr TAC	Tyr TAT	Arg CGT	Gln CAA	Gly GGC	Cys TGT	1950
Ala GCC	Ser TCC	Lys AAA	Leu CTG	Pro CCT	Val GTC	Lys AAG	Trp TGG	Leu CTG	Ala GCC	Leu CTG	Glu GAG	Ser AGC	1989
Leu CTG	Ala GCC	Asp GAC	Asn AAC	Leu CTG	Tyr TAT	Thr ACT	Val GTG	Gln CAG	Ser AGT	Asp GAC	Val GTG	Trp TGG	2028
Ala GCG	Phe TTC	Gly GGG	Val GTG	Thr ACC	Met ATG	Trp TGG	Glu GAG	Ile ATC	Met ATG	Thr ACA	Arg CGT	Gly GGG	2067
Gln CAG	Thr ACG	Pro CCA	Tyr TAT	Ala GCT	Gly GGC	Ile ATC	Glu GAA	Asn AAC	Ala GCT	Glu GAG	Ile ATT	Tyr TAC	2106
Asn AAC	Tyr TAC	Leu CTC	Ile ATT	Gly GGC	Gly GGG	Asn AAC	Arg CGC	Leu CTG	Lys AAA	Gln CAG	Pro CCT	Pro CCG	2145
Glu GAG	Cys TGT	Met ATG	Glu GAG	Asp GAC	Val GTG	Tyr TAT	Asp GAT	Leu CTC	Met ATG	Tyr TAC	Gln CAG	Cys TGC	2184
Trp TGG	Ser AGT	Ala GCT	Asp GAC	Pro CCC	Lys AAG	Gln CAG	Arg CGC	Pro CCG	Ser AGC	Phe TTT	Thr ACT	Cys TGT	2223
Leu CTG	Arg CGA	Met ATG	Glu GAA	Leu CTG	Glu GAG	Asn AAC	Ile ATC	Leu TTG	Gly GGC	Gln CAG	Leu CTG	Ser TCT	2262
Val GTG	Leu CTA	Ser TCT	Ala GCC	Ser AGC	Gln CAG	Asp GAC	Pro CCC	Leu TTA	Tyr TAC	Ile ATC	Asn AAC	Ile ATC	2301
Glu GAG	Arg AGA	Ala GCT	Glu GAG	Glu GAG	Pro CCC	Thr ACT	Val GTG	Gly GGA	Gly GGC	Ser AGC	Leu CTG	Glu GAG	2340

Leu	Pro	Gly	Arg	Asp	Gln	Pro	Tyr	Ser	Gly	Ala	Gly	Asp	2379
CTA	CCT	GGC	AGG	GAT	CAG	CCC	TAC	AGT	GGG	GCT	GGG	GAT	
Gly	Ser	Gly	Met	Gly	Ala	Val	Gly	Gly	Thr	Pro	Ser	Asp	2418
GGC	AGT	GGC	ATG	GGG	GCA	GTG	GGT	GGC	ACT	CCC	AGT	GAC	
Cys	Arg	Tyr	Ile	Leu	Thr	Pro	Gly	Gly	Leu	Ala	Glu	Gln	2457
TGT	CGG	TAC	ATA	CTC	ACC	CCC	GGA	GGG	CTG	GCT	GAG	CAG	
Pro	Gly	Gln	Ala	Glu	His	Gln	Pro	Glu	Ser	Pro	Leu	Asn	2496
CCA	GGG	CAG	GCA	GAG	CAC	CAG	CCA	GAG	AGT	CCC	CTC	AAT	
Glu	Thr	Gln	Arg	Leu	Leu	Leu	Leu	Gln	Gln	Gly	Leu	Leu	2535
GAG	ACA	CAG	AGG	CTT	TTG	CTG	CTG	CAG	CAA	GGG	CTA	CTG	
Pro	His	Ser	Ser	Cys									2550
CCA	CAC	AGT	AGC	TGT									

(12) INFORMATION FOR SEQUENCE ID NO. 11:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1158 BASE PAIRS

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: cDNA

(3) SEQUENCE DESCRIPTION: SEQ ID NO. 11:

											Ala	Gly	6
											GCA	GGC	
Leu	Lys	Leu	Met	Gly	Ala	Pro	Val	Lys	Met	Thr	Val	Ser	45
CTG	AAG	CTC	ATG	GGC	GCC	CCA	GTG	AAG	ATG	ACC	GTG	TCT	
Gln	Gly	Gln	Pro	Val	Lys	Leu	Asn	Cys	Ser	Val	Glu	Gly	84
CAG	GGG	CAG	CCA	GTG	AAG	CTC	AAC	TGC	AGC	GTG	GAG	GGG	
Met	Glu	Asp	Pro	Asp	Ile	His	Trp	Met	Lys	Asp	Gly	Thr	123
ATG	GAG	GAC	CCT	GAC	ATC	CAC	TGG	ATG	AAG	GAT	GGC	ACC	
Val	Val	Gln	Asn	Ala	Ser	Gln	Val	Ser	Ile	Ser	Ile	Ser	162
GTG	GTC	CAG	AAT	GCA	AGC	CAG	GTG	TCC	ATC	TCC	ATC	AGC	
Glu	His	Ser	Trp	Ile	Gly	Leu	Leu	Ser	Leu	Lys	Ser	Val	201
GAG	CAC	AGC	TGG	ATT	GGC	TTA	CTC	AGC	CTA	AAG	TCA	GTG	
Glu	Arg	Ser	Asp	Ala	Gly	Leu	Tyr	Trp	Cys	Gln	Val	Lys	240
GAG	CGG	TCT	GAT	GCT	GGC	CTG	TAC	TGG	TGC	CAG	GTG	AAG	
Asp	Gly	Glu	Glu	Thr	Lys	Ile	Ser	Gln	Ser	Val	Trp	Leu	279
GAT	GGG	GAG	GAA	ACC	AAG	ATC	TCT	CAG	TCA	GTA	TGG	CTC	
Thr	Val	Glu	Gly	Val	Pro	Phe	Phe	Thr	Val	Glu	Pro	Lys	318
ACT	GTC	GAA	GGT	GTG	CCA	TTC	TTC	ACA	GTG	GAA	CCA	AAA	
Asp	Leu	Ala	Val	Pro	Pro	Asn	Ala	Pro	Phe	Gln	Leu	Ser	357
GAT	CTG	GCG	GTG	CCA	CCC	AAT	GCC	CCT	TTT	CAG	CTG	TCT	
Cys	Glu	Ala	Val	Gly	Pro	Pro	Glu	Pro	Val	Thr	Ile	Tyr	396
TGT	GAG	GCT	GTG	GGT	CCT	CCA	GAA	CCC	GTA	ACC	ATT	TAC	

Trp	Trp	Arg	Gly	Leu	Thr	Lys	Val	Gly	Gly	Pro	Ala	Pro	435
TGG	TGG	AGA	GGA	CTC	ACT	AAA	GTT	GGG	GGA	CCT	GCT	CCC	
Ser	Pro	Ser	Val	Leu	Asn	Val	Thr	Gly	Val	Thr	Gln	Arg	474
TCT	CCC	TCT	GTT	TTA	AAT	GTG	ACG	GGA	GTG	ACC	CAG	CGC	
Thr	Glu	Phe	Ser	Cys	Glu	Ala	Arg	Asn	Ile	Lys	Gly	Leu	513
ACA	GAG	TTT	TCT	TGT	GAA	GCC	CGC	AAC	ATA	AAA	GGC	CTG	
Ala	Thr	Ser	Arg	Pro	Ala	Ile	Val	Arg	Leu	Gln	Ala	Pro	552
GCC	ACT	TCC	CGA	CCA	GCC	ATT	GTT	CGC	CTT	CAA	GCA	CCG	
Pro	Ala	Ala	Pro	Phe	Asn	Thr	Thr	Val	Thr	Thr	Ile	Ser	591
CCT	GCA	GCT	CCT	TTC	AAC	ACC	ACA	GTA	ACA	ACG	ATC	TCC	
Ser	Tyr	Asn	Ala	Ser	Val	Ala	Trp	Val	Pro	Gly	Ala	Asp	630
AGC	TAC	AAC	GCT	AGC	GTG	GCC	TGG	GTG	CCA	GGT	GCT	GAC	
Gly	Leu	Ala	Leu	Leu	His	Ser	Cys	Thr	Val	Gln	Val	Ala	669
GGC	CTA	GCT	CTG	CTG	CAT	TCC	TGT	ACT	GTA	CAG	GTG	GCA	
His	Ala	Pro	Gly	Glu	Trp	Glu	Ala	Leu	Ala	Val	Val	Val	708
CAC	GCC	CCA	GGA	GAA	TGG	GAG	GCC	CTT	GCT	GTT	GTG	GTT	
Pro	Val	Pro	Pro	Phe	Thr	Cys	Leu	Leu	Arg	Asn	Leu	Ala	747
CCT	GTG	CCA	CCT	TTT	ACC	TGC	CTG	CTT	CGG	AAC	TTG	GCC	
Pro	Ala	Thr	Asn	Tyr	Ser	Leu	Arg	Val	Arg	Cys	Ala	Asn	786
CCT	GCC	ACC	AAC	TAC	AGC	CTT	AGG	GTG	CGC	TGT	GCC	AAT	
Ala	Leu	Gly	Pro	Ser	Pro	Tyr	Gly	Asp	Trp	Val	Pro	Phe	825
GCC	TTG	GGC	CCT	TCT	CCC	TAC	GGC	GAC	TGG	GTG	CCC	TTT	
Gln	Thr	Lys	Gly	Leu	Ala	Pro	Ala	Arg	Ala	Pro	Gln	Asn	864
CAG	ACA	AAG	GGC	CTA	GCG	CCA	GCC	AGA	GCT	CCT	CAG	AAT	
Phe	His	Ala	Ile	Arg	Thr	Asp	Ser	Gly	Leu	Ile	Leu	Glu	903
TTC	CAT	GCC	ATT	CGT	ACC	GAC	TCA	GGC	CTT	ATC	CTG	GAA	
Trp	Glu	Glu	Val	Ile	Pro	Glu	Asp	Pro	Gly	Glu	Gly	Pro	941
TGG	GAA	GAA	GTG	ATT	CCT	GAG	GAC	CCT	GGG	GAA	GGC	CCC	
Leu	Gly	Pro	Tyr	Lys	Leu	Ser	Trp	Val	Gln	Glu	Asn	Gly	981
CTA	GGA	CCT	TAT	AAG	CTG	TCC	TGG	GTC	CAA	GAA	AAT	GGA	
Thr	Gln	Asp	Glu	Leu	Met	Val	Glu	Gly	Thr	Arg	Ala	Asn	1020
ACC	CAG	GAT	GAG	CTG	ATG	GTG	GAA	GGG	ACC	AGG	GCC	AAT	
Leu	Thr	Asp	Trp	Asp	Pro	Gln	Lys	Asp	Leu	Ile	Leu	Arg	1059
CTG	ACC	GAC	TGG	GAT	CCC	CAG	AAG	GAC	CTG	ATT	TTG	CGT	
Val	Cys	Ala	Ser	Asn	Ala	Ile	Gly	Asp	Gly	Pro	Trp	Ser	1098
GTG	TGT	GCC	TCC	AAT	GCA	ATT	GGT	GAT	GGG	CCC	TGG	AGT	
Gln	Pro	Leu	Val	Val	Ser	Ser	His	Asp	His	Ala	Gly	Arg	1137
CAG	CCA	CTG	GTG	GTG	TCT	TCT	CAT	GAC	CAT	GCA	GGG	AGG	
Gln	Gly	Pro	Pro	His	Ser	Arg							1158
CAG	GGC	CCT	CCC	CAC	AGC	CGC							

(13) INFORMATION FOR SEQUENCE ID NO. 12:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1158 BASE PAIRS

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: cDNA

(3) SEQUENCE DESCRIPTION: SEQ ID NO. 12:

Ala	Gly	Leu	Lys	Leu	Met	Gly	Ala	Pro	Val	Lys	Leu	Thr	39
GCA	GGT	CTG	AAG	CTC	ATG	GGA	GCC	CCG	GTG	AAG	CTG	ACA	
Val	Ser	Gln	Gly	Gln	Pro	Val	Lys	Leu	Asn	Cys	Ser	Val	78
GTG	TCT	CAG	GGG	CAG	CCG	GTG	AAG	CTC	AAC	TGC	AGT	GTG	
Glu	Gly	Met	Glu	Glu	Pro	Asp	Ile	Gln	Trp	Val	Lys	Asp	117
GAG	GGG	ATG	GAG	GAG	CCT	GAC	ATC	CAG	TGG	GTG	AAG	GAT	
Gly	Ala	Val	Val	Gln	Asn	Leu	Asp	Gln	Leu	Tyr	Ile	Pro	156
GGG	GCT	GTG	GTC	CAG	AAC	TTG	GAC	CAG	TTG	TAC	ATC	CCA	
Val	Ser	Glu	Gln	His	Trp	Ile	Gly	Phe	Leu	Ser	Leu	Lys	195
GTC	AGC	GAG	CAG	CAC	TGG	ATC	GGC	TTC	CTC	AGC	CTG	AAG	
Ser	Val	Glu	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Trp	Cys	Gln	234
TCA	GTG	GAG	CGC	TCT	GAC	GCC	GGC	CGG	TAC	TGG	TGC	CAG	
Val	Glu	Asp	Gly	Gly	Glu	Thr	Glu	Ile	Ser	Gln	Pro	Val	273
GTG	GAG	GAT	GGG	GGT	GAA	ACC	GAG	ATC	TCC	CAG	CCA	GTG	
Trp	Leu	Thr	Val	Glu	Gly	Val	Pro	Phe	Phe	Thr	Val	Glu	312
TGG	CTC	ACG	GTA	GAA	GGT	GTG	CCA	TTT	TTC	ACA	GTG	GAG	
Pro	Lys	Asp	Leu	Ala	Val	Pro	Pro	Asn	Ala	Pro	Phe	Gln	351
CCA	AAA	GAT	CTG	GCA	GTG	CCA	CCC	AAT	GCC	CCT	TTC	CAA	
Leu	Ser	Cys	Glu	Ala	Val	Gly	Pro	Pro	Glu	Pro	Val	Thr	390
CTG	TCT	TGT	GAG	GCT	GTG	GGT	CCC	CCT	GAA	CCT	GTT	ACC	
Ile	Val	Trp	Trp	Arg	Gly	Thr	Thr	Lys	Ile	Gly	Gly	Pro	429
ATT	GTC	TGG	TGG	AGA	GGA	ACT	ACG	AAG	ATC	GGG	GGA	CCC	
Ala	Pro	Ser	Pro	Ser	Val	Leu	Asn	Val	Thr	Gly	Val	Thr	468
GCT	CCC	TCT	CCA	TCT	GTT	TTA	AAT	GTA	ACA	GGG	GTG	ACC	
Gln	Ser	Thr	Met	Phe	Ser	Cys	Glu	Ala	His	Asn	Leu	Lys	507
CAG	AGC	ACC	ATG	TTT	TCC	TGT	GAA	GCT	CAC	AAC	CTA	AAA	
Gly	Leu	Ala	Ser	Ser	Arg	Thr	Ala	Thr	Val	His	Leu	Gln	546
GGC	CTG	GCC	TCT	TCT	CGC	ACA	GCC	ACT	GTT	CAC	CTT	CAA	
Ala	Leu	Pro	Ala	Ala	Pro	Phe	Asn	Ile	Thr	Val	Thr	Lys	585
GCA	CTG	CCT	GCA	GCC	CCC	TTC	AAC	ATC	ACC	GTG	ACA	AAG	
Leu	Ser	Ser	Ser	Asn	Ala	Ser	Val	Ala	Trp	Met	Pro	Gly	624
CTT	TCC	AGC	AGC	AAC	GCT	AGT	GTG	GCC	TGG	ATG	CCA	GGT	
Ala	Asp	Gly	Arg	Ala	Leu	Leu	Gln	Ser	Cys	Thr	Val	Gln	663
GCT	GAT	GGC	CGA	GCT	CTG	CTA	CAG	TCC	TGT	ACA	GTT	CAG	
Val	Thr	Gln	Ala	Pro	Gly	Gly	Trp	Glu	Val	Leu	Ala	Val	702
GTG	ACA	CAG	GCC	CCA	GGA	GGC	TGG	GAA	GTC	CTG	GCT	GTT	
Val	Val	Pro	Val	Pro	Pro	Phe	Thr	Cys	Leu	Leu	Arg	Asp	741
GTG	GTC	CCT	GTG	CCC	CCC	TTT	ACC	TGC	CTG	CTC	CGG	GAC	
Leu	Val	Pro	Ala	Thr	Asn	Tyr	Ser	Leu	Arg	Val	Arg	Cys	780
CTG	GTG	CCT	GCC	ACC	AAC	TAC	AGC	CTC	AGG	GTG	CGC	TGT	

Ala GCC	Asn AAT	Ala GCC	Leu TTG	Gly GGG	Pro CCC	Ser TCT	Pro CCC	Tyr TAT	Ala GCT	Asp GAC	Trp TGG	Val GTG	819
Pro CCC	Phe TTT	Gln CAG	Thr ACC	Lys AAG	Gly GGT	Leu CTA	Ala GCC	Pro CCA	Ala GCC	Ser AGC	Ala GCT	Pro CCC	858
Gln CAA	Asn AAC	Leu CTC	His CAT	Ala GCC	Ile ATC	Arg CGC	Thr ACA	Asp GAT	Ser TCA	Gly GGC	Leu CTC	Ile ATC	897
Leu TTG	Glu GAG	Trp TGG	Glu GAA	Glu GAA	Val GTG	Ile ATC	Pro CCC	Glu GAG	Ala GCC	Pro CCT	Leu TTG	Glu GAA	936
Gly GGC	Pro CCC	Leu CTG	Gly GGA	Pro CCC	Tyr TAC	Lys AAA	Leu CTG	Ser TCC	Trp TGG	Val GTT	Gln CAA	Asp GAC	975
Asn AAT	Gly GGA	Thr ACC	Gln CAG	Asp GAT	Glu GAG	Leu CTG	Thr ACA	Val GTG	Glu GAG	Gly GGG	Thr ACC	Arg AGG	1014
Ala GCC	Asn AAT	Leu TTG	Thr ACA	Gly GGC	Trp TGG	Asp GAT	Pro CCC	Gln CAA	Lys AAG	Asp GAC	Leu CTG	Ile ATC	1053
Val GTA	Arg CGT	Val GTG	Cys TGC	Val GTC	Ser TCC	Asn AAT	Ala GCA	Val GTT	Gly GGC	Cys TGT	Gly GGA	Pro CCC	1092
Trp TGG	Ser AGT	Gln CAG	Pro CCA	Leu CTG	Val GTG	Val GTC	Ser TCT	Ser TCT	His CAT	Asp GAC	Arg CGT	Ala GCA	1131
Gly GGC	Gln CAG	Gln CAG	Gly GGC	Pro CCT	Pro CCT	His CAC	Ser AGC	Arg CGC					1158

CLAIMS:

1. A mammalian receptor tyrosine kinase which is a developmental tyrosine kinase (Dtk) and which is expressed in multipotential haematopoietic cells, in embryonic stem cells, in brain tissue and in testis, but which is not expressed in mature lineage-restricted haematopoietic cells.
2. A receptor tyrosine kinase according to claim 1 that is murine Dtk having the amino acid sequence of SEQ ID NO 1, or a functional equivalent thereof.
3. A receptor tyrosine kinase according to claim 1 that is mature murine Dtk having the amino acid sequence of SEQ ID NO 2.
4. A receptor tyrosine kinase according to claim 1 that is human Dtk having the amino acid sequence of SEQ ID NO 3, or a functional equivalent thereof.
5. A receptor tyrosine kinase according to claim 1 that is mature human Dtk having the amino acid sequence of SEQ ID NO 4.
6. An extracellular receptor domain of a receptor tyrosine kinase according to claim 1.
7. An extracellular receptor domain which is the extracellular receptor domain of mature murine Dtk as defined in claim 3, or a functional equivalent thereof.
8. An extracellular receptor domain of a receptor tyrosine kinase having the amino acid sequence of SEQ ID NO 5.
9. An extracellular receptor domain which is the extracellular receptor domain of mature human Dtk as defined in claim 5, or a functional equivalent thereof.
10. An extracellular receptor domain of a receptor tyrosine kinase having the amino acid sequence of SEQ ID NO 6.

11. An extracellular receptor domain according to any one of claims 6 to 10 which is bound or attached to a support.
- 5 12. A soluble receptor comprising the extracellular receptor domain of a receptor tyrosine kinase according to any one of claims 1 to 5 lacking the transmembrane region and catalytic domain of said receptor tyrosine kinase.
- 10 13. A nucleic acid molecule encoding a receptor tyrosine kinase as defined in claim 1.
14. A nucleic acid molecule encoding murine Dtk or a functional equivalent thereof as defined in claim 2.
- 15 15. A nucleic acid molecule according to claim 14 which is DNA.
16. A DNA molecule according to claim 15 having the nucleotide sequence of SEQ ID NO 7.
- 20 17. A nucleic acid molecule encoding mature murine Dtk as defined in claim 3.
18. A nucleic acid molecule according to claim 17 which is DNA.
- 25 19. A DNA molecule according to claim 18 having the nucleotide sequence of SEQ ID NO 8.
20. A nucleic acid molecule encoding human Dtk or a functional equivalent thereof as defined in claim 4.
- 30 21. A nucleic acid molecule according to claim 20 which is DNA.
22. A DNA molecule according to claim 21 having the nucleotide sequence of SEQ ID NO 9.

23. A nucleic acid molecule encoding mature human Dtk as defined in claim 5.

24. A nucleic acid molecule according to claim 23 which is DNA.

5 25. A DNA molecule according to claim 24 having the nucleotide sequence of SEQ ID NO 10.

26. A nucleic acid molecule encoding an extracellular receptor domain as defined in claim 6.

10

27. A nucleic acid molecule encoding the extracellular receptor domain of murine Dtk or a functional equivalent thereof as defined in claim 7.

28. A nucleic acid molecule according to claim 27 which is DNA.

15

29. A DNA molecule according to claim 28 having the nucleotide sequence of SEQ ID NO 11.

20

30. A nucleic acid molecule encoding the extracellular receptor domain of human Dtk or a functional equivalent thereof as defined in claim 9.

31. A nucleic acid molecule according to claim 30 which is DNA.

25

32. A DNA molecule according to claim 31 having the nucleotide sequence of SEQ ID NO 12.

33. A vector including a DNA molecule as defined in claim 13.

30

34. A vector including a DNA molecule as defined in any one of claims 15, 16, 18 and 19.

35. A vector including a DNA molecule as defined in any one of claims 21, 22, 24 and 25.

36. A vector including a DNA molecule as defined in claim 28 or claim 29.
37. A vector including a DNA molecule as defined in claim 31 or claim 32.
- 5 38. A method of producing a receptor tyrosine kinase comprising the steps of:
(a) culturing a host cell which has been transformed or transfected with a vector as claimed in any one of claims 33-35 to express the encoded receptor tyrosine kinase; and
(b) recovering the expressed receptor tyrosine kinase.
- 10 39. A method of producing an extracellular receptor domain of a receptor tyrosine kinase comprising the steps of:
(a) culturing a host cell which has been transformed or transfected with a vector as claimed in claim 36 or claim 37 to express the encoded
15 extracellular receptor domain; and
(b) recovering the expressed extracellular receptor domain.
- 20 40. A recombinant receptor tyrosine kinase which is the product of a method as defined in claim 38.
41. A recombinant extracellular receptor domain which is the product of a method as defined in claim 39.
- 25 42. A ligand that binds to a receptor tyrosine kinase as defined in claim 1.
43. A ligand that binds to a receptor tyrosine kinase as defined in claim 2.
44. A ligand that binds to a receptor tyrosine kinase as defined in claim 3.
- 30 45. A ligand that binds to a receptor tyrosine kinase as defined in claim 4.
46. A ligand that binds to a receptor tyrosine kinase as defined in claim 5.

47. A ligand that binds to an extracellular receptor domain of a receptor tyrosine kinase as defined in claim 6.

5 48. A ligand that binds to an extracellular receptor domain of a receptor tyrosine kinase as defined in claim 7.

49. A ligand that binds to an extracellular receptor domain of a receptor tyrosine kinase as defined in claim 8.

10 50. A ligand that binds to an extracellular receptor domain of a receptor tyrosine kinase as defined in claim 9.

51. A ligand that binds to an extracellular receptor domain of a receptor tyrosine kinase as claimed in claim 10.

15 52. A ligand that binds to an extracellular receptor domain of a receptor tyrosine kinase as claimed in claim 11.

53. A ligand that binds to a soluble receptor as defined in claim 12.

20 54. A ligand that binds to a receptor tyrosine kinase as claimed in claim 40.

55. A ligand that binds to an extracellular receptor domain as claimed in claim 41.

25 56. A ligand according to any one of claims 42-55 wherein the ligand stimulates the proliferation, differentiation and/or survival of cells which express a receptor tyrosine kinase according to claim 1.

30 57. A ligand according to any one of claims 42-55 wherein the ligand is antagonistic and at least partially blocks or inhibits the function of a receptor tyrosine kinase according to claim 1 through binding to said receptor.

58. A method of stimulating the proliferation, differentiation and/or survival of a cell expressing a receptor tyrosine kinase according to claim 1 comprising contacting the cell with a ligand according to claim 56.

5 59. A method according to claim 58 wherein the stimulation occurs *in vivo*.

60. A method according to claim 58 wherein the stimulation occurs *ex vivo*.

10 61. A method of inhibiting the function of a receptor tyrosine kinase according to claim 1 comprising contacting the receptor with a ligand according to claim 57.

62. A method according to claim 61 wherein the inhibition occurs *in vivo*.

15 63. A method according to claim 61 wherein the inhibition occurs *ex vivo*.

64. A method of treating a disease, syndrome or condition caused or mediated by an excess of a ligand as claimed in claim 56 comprising the step of contacting said excess of said ligand with an effective amount of a receptor tyrosine kinase according to any one of claims 1-5 and 40, an extracellular receptor domain according to any one of claims 6-11 and 41 or a soluble receptor according to claim 12.

20

65. A method of treating a disease, syndrome or condition caused or mediated by an excess of a ligand as defined in claim 57 comprising the step of contacting said excess of said ligand with an effective amount of a receptor tyrosine kinase according to any one of claims 1-5 and 40, an extracellular receptor domain according to any one of claims 6-11 and 41 or a soluble receptor according to claim 12.

25

30 66. A method of extracting a ligand as defined in claim 56 or claim 57 from a medium which may contain said ligand comprising the step of contacting said medium with a receptor tyrosine kinase according to any one of claims 1-5 and 40,

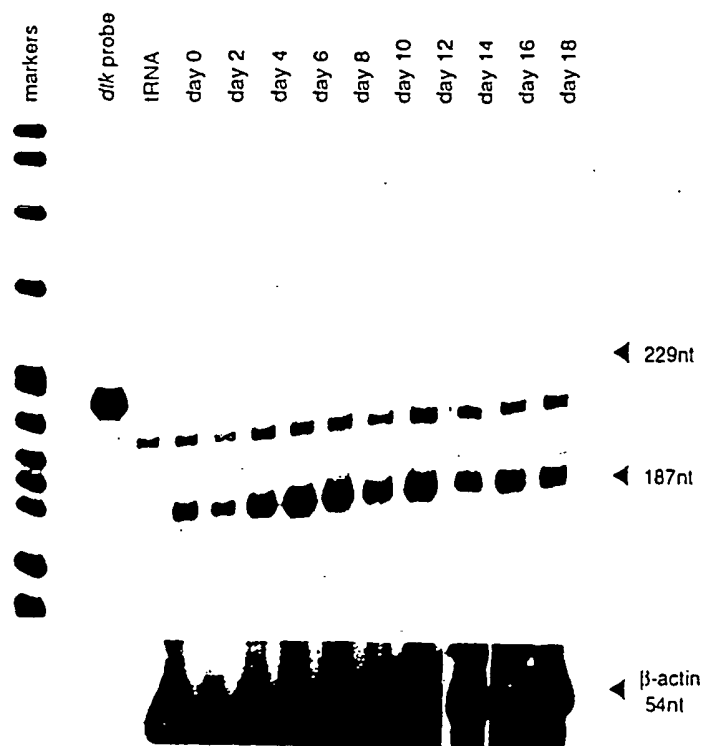
an extracellular receptor domain according to any one of claims 6-11 and 41 or a soluble receptor according to claim 12.

5 67. A method of isolating ligand(s) as defined in claim 56 or claim 57 from a medium which may contain said ligand(s), comprising the steps of:

- (a) contacting said medium with an effective amount of a receptor tyrosine kinase according to any one of claims 1-5 and 40, an extracellular domain according to any one of claims 6-11 and 41 or a soluble receptor according to claim 12;
- 10 (b) detecting which ligand(s) bind to said tyrosine kinase receptor, extracellular receptor domain or soluble receptor; and
- (c) isolating such bound ligand(s).

68. A ligand which is isolated by a method according to claim 67.

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FIG 1

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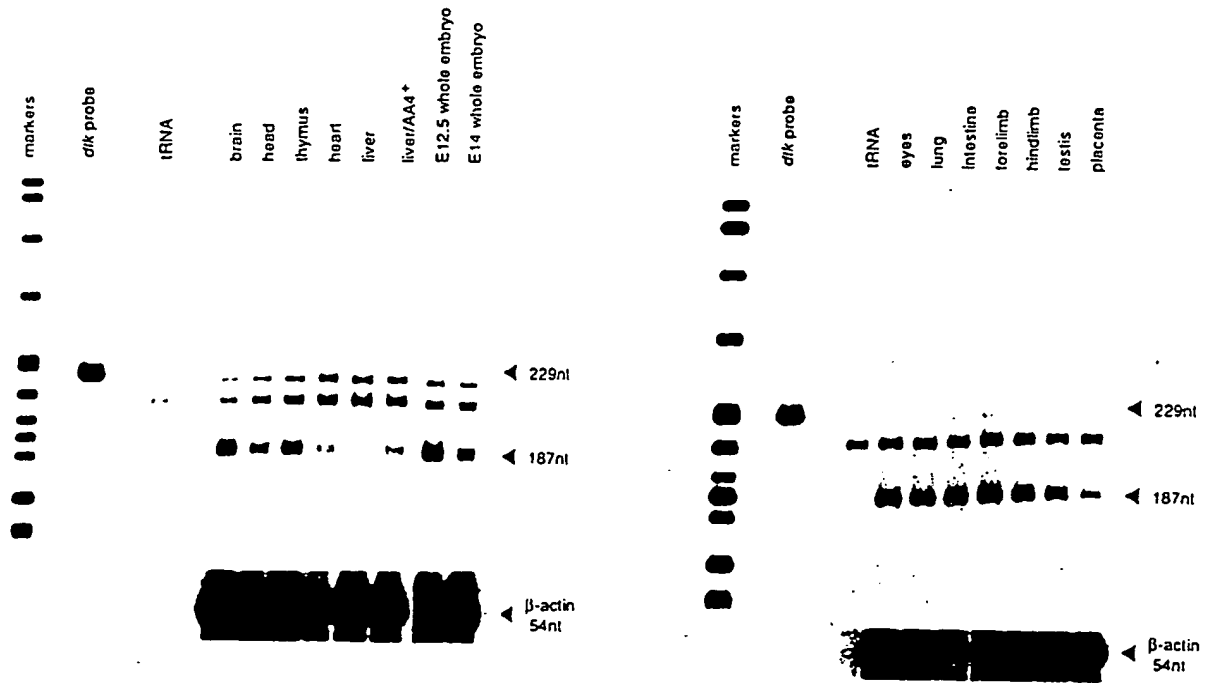
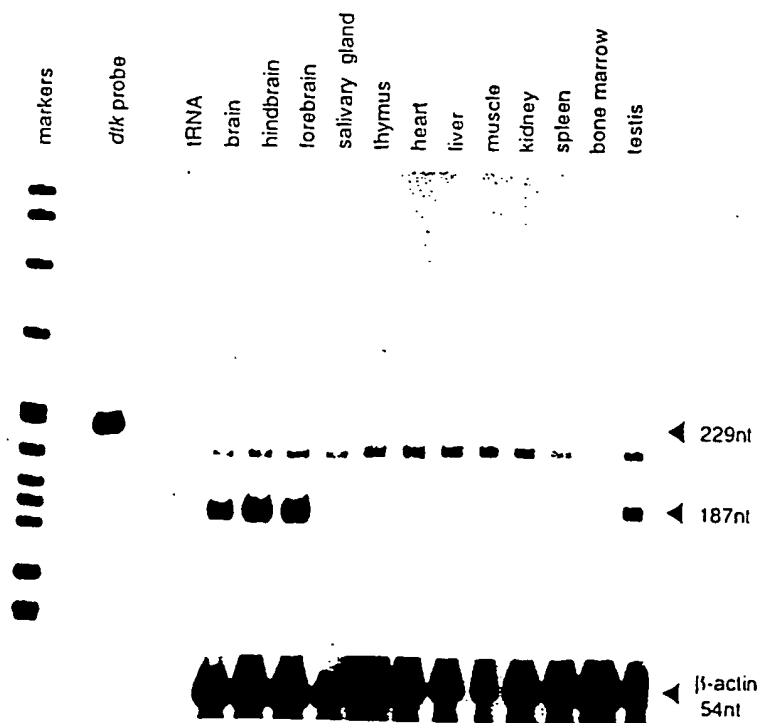


FIG 2

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FIG 3

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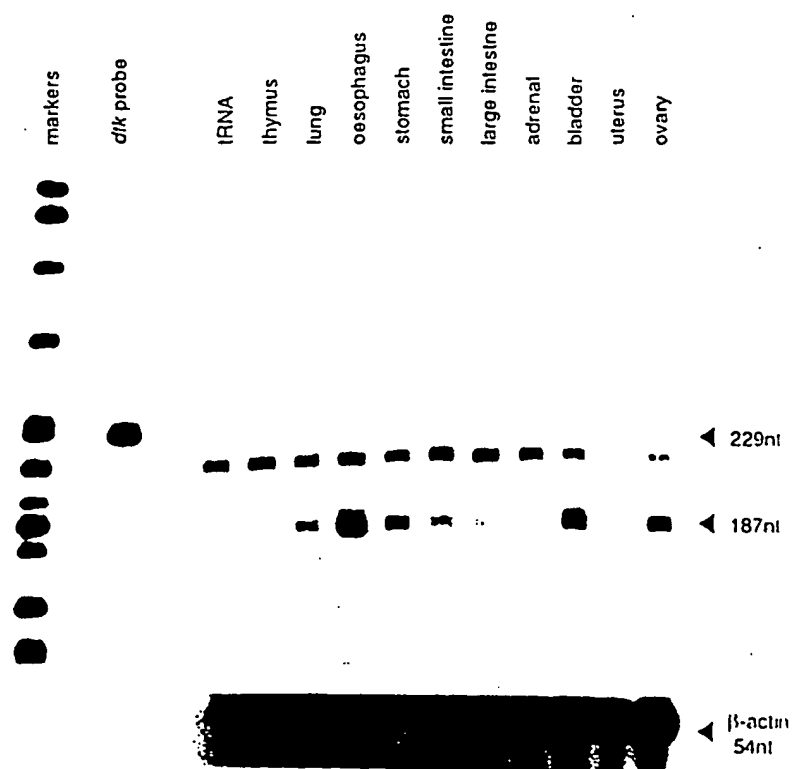
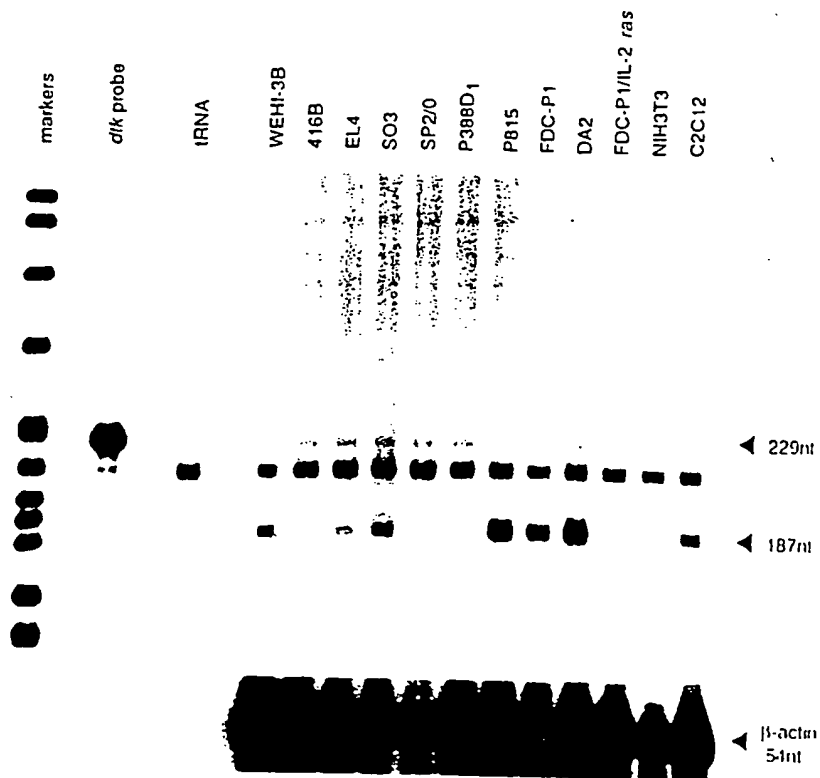


FIG 4

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FIG 5

IG 6 (cont)

CATTAGATCTTTACATGAAAGTAAATTTATAAGATTTCTAGAAAAGTCAAAAGATGAATCTATTTCTTAGGATACTAAAGCACTCACATTATAGAAA 100
 AAATCAGTTAACTACTCCACAAACATTTAAAGGCTCCCTATAAAAAACATTTTAAATAGCAAGCCACAGAAAGGCAAAATATTAATAGTTTGCAT 200
 ACATATGTAAGAAAAGCAATTTGAATCTAGAATATTTAAACAAAGCTTTTACAACTCAAAATAACAAAGAAATATTTTCTTCCAAATTTGGCAAAATTA 300
 AACAGAACCTTCACAAAGAAAGATGAATGTTTAAATAACATTTTGAAGCCATAATNATGACATCATTAAGCCATGATGGAATGCNAATTTAAGTACCAC 400
 TTACATCCACAGAAAACATAAATAAAGGACTGAGCTCACCAAAATTTGGTGAAGATGTGGTAATACGAAATTTCTGTACCGTGTCTCTGAGGG 500
 TATAACATATACAGGATTTTGTGAATACTAGTGGTTCTCTTATATAAATTAATGCTTGGCAACCTATTTACTTAAGAATGAAGGGGCCCGC 600
 CCTCTCCCTCTCTCGCTCGGGGCCCGGCATGCTGGCGCTCCCGCGATGCGCTGAGGCGAGCATGGGCGCGCGGCTCCCGCGCTGC 700
 L P P P R L G L L A E S A A A G L K L M G A P V K L T V S Q G
 CGTGGCGGCCACCGCGCTCGCTGGCGAGTCCGCCCGGAGGTCTGAAGCTCATGGGAGCCCGGTGAAGCTGACAGTGTCTCAGGG 800
 Q P V K L N C S V E G M E E P D I Q W V K D G A V V Q N L D Q L Y
 GACGCGGTGAAGCTCAACTGCACTGAGGGGATGGAGGAGCTCACATCCAGTGGGTGAAGGATGGGGCTGTGGTCCAGAACTTGGACCAGTTGTAC 900
 I P V S E Q H W I G F L S L K S V E R S D A G R Y W C Q V E D G G E
 ATCCAGTCAGCAGCAGCACTGGATCGGCTTCTCAGCTCAGCTGAGTGGAGCGCTCTGACGCGCGCGCTACTGGTGGCAGGTGGAGGATGGGGTG 1000
 T E I S Q P V W L T V E G V P F F T V E P K D L A V P P N A P F Q
 AAACCGAGATCTCCAGCCAGTGTGGCTCACGCTAGAGGTGTGCCATTTTTCACAGTGGAGCAAAAGATCTGGCAGTGGCCAGTGGCCCAATGCCCTTTCCA 1100
 L S C E A V G P P E P V T I V W W R G T T K I G G P A P S P S V L
 ACTGTCTGTGAGGCTGGCTGAACTGTACCATTTGTCTGGTGGAGAGGAATACGAAGATCGGGGAGCCCGCTCCCTCTCCATCTGTCTTTA 1200
 N V T G V T Q S T M F S C E A H N L K G L A S R T A T V H L Q A L
 AATGTAAACAGGGGTGACCCAGACCATGTTTCTGTGAAGCTCACAACTTAAAGGCTTGGCTCTCTGACAGCACTGTTCACCTTCAAGCAC 1300
 P A A P F N I T V T K L S S S N A S V A W M P G A D G R A L L Q S
 TGCCTGCAGCCCCCTTCAACATCACCGTGACAAAGCTTTCACAGCAGCAACGCTAGTGTGGCTGGATGCCAGTGTGGCCGAGCTCTGCTACAGTC 1400
 C T V Q V T Q A P G G W E V L A V V V P P P F T C L L R D L V P
 CTGTACAGTTACAGTGACAGAGCCCGCAGGAGGCTGGCAAGTCTCTGGCTGTGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
 A T N Y S L R V R C A N A L G P S P Y A D W V P F Q T K G L A P A S
 GCCACCAACTACAGCCTCAGGTGGCTGTGCAATGCTTGGGCGCTCTCCCTATGCTGACTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1600
 A P Q N L H A I R T D S G L I L E W E E V I P E A P L E G P L G P
 GCGTCCCCAAACCTCCATGCCATCCACAGATTCAGGCTCTATTTGGAGTGGAGGAAGATGCCCGAGGCCCTTTGGAGGCCCTTGGGACC 1700
 Y K L S W V Q D N G T Q D E L T V E G T R A N L T G W D P Q K D L
 CTACAACTGCTGGTTCAACACAAATGGAACCCAGATGAGCTGACAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1800
 I V R V C V S N A V G C G P W S Q P L V V S S H D R A G O Q G P P H
 ATCGTACGTGTGCTCCAAATGAGTGGCTGTGGACCTGTGGAGTCAAGCACTGTGTGTCTCTCTCATGACGCTGACGCGGAGGAGGAGGAGGAGGAGG 1900
 S R T S W V P V L G V L T A L V T A A A L A L I L L R K R K E
 ACAGCCGCATCTCTGGGTACCTTGGTGTCTTACGCCCTTACGCCCTTACGCCCTTACGCCCTTACGCCCTTACGCCCTTACGCCCTTACGCCCTTACGCC 2000
 T R F G Q A F D S V M A R G E P A V H F R A A R S F N R E R P E R
 GACGCGTTTGGCAAGCCTTTGACAGTGTATGGCCCGGGAGAGCAGCGCTTCACTTCCGGGAGCGCCGCTTCAATCAGAGAAAGGCCGAGCGC 2100

